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GenCore version 5.1.6
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February 15, 2004, 05:50:07; Search time 18600 Seconds (without alignments) 11619.654 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 CVE18316 LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL

	3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		3731 CTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGT 3790 2974 CTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGAGCT 3033 3791 TATC
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Direct Submission Direct Submission Submitted (30-007-1998) D. Bannasch, Institution Division of, Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im Neuenheimer Feld 280, D-69120 Heidelberg, FRG Revised by author 10-UNN-1999 Related sequences U07646, U00004, L19385. Location/Qualifiers 1. 6074 / mol_type="genomic DNA" / Mol_type="genomic DNA" / Mol_type="genomic DNA" / Abxref="taxon:91498" / Abzref="taxon:91498" / note="ORFI" / codon_start=1 / product="hypothetical protein" / product="hypothetical protein"		/procein_is="CAB54528_1" / db_xref="G1="CAB54528_1" / db_xref="G1="CAB54528_1" / translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR / translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR PVLEVYTDLGSGALNELQDBARLSWLATTGYPCAAVLDVYTRAGRDWLLIGEVPGQDL LSSHLAPAEKVSIMADAWRRLHTLDPATTGFPDHQAKHRIERARTRMEAGLVDQDDLDE EHQGLAPAELFARLKARPDGEDLVVTHGDACLPNINVENGRFSGFIDGGRLGVADRY QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF" complement (44104459) /gene="aminoglycoside phosphotransferase" /gene="aminoglycoside phosphotransferase" /gene="aminoglycoside phosphotransferase" /gene="aminoglycoside phosphotransferase" /gene="aminoglycoside phosphotransferase"	# 45.6%; Score 2410; DB 12; Length 6074; S8: Conservative 0; Mismatches 5; Indels 145; Gaps 1; CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 2770 # CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 2770 ## CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 2013 ## ACATACGAGCCGAAAGCATAAAGTGTAAAAGCTGGGGTGCCTAATGAGTGAG
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Oy 5026 AGGGCTTCCCAACCTTACCAGAGGCCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCC 5085 4114 AGGGCTTCCCAACCTTACCAGAGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGCTGTCC 473 CONSTRUCT ATAAAACCCCCAGTCTAGCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCT 5145 A474 ATAAAAACCCCCCAGTTAGCTATCGCCATGCTAGCTACCTGCTTTCTCT 4533 Oy 5146 ATGCGCTTGCGGTTTTCCCTTGTAGCTACCCAGTAGCTGCAGCTACCTGCTTTCTCT 4533 Db 4534 TTGCGCTTGCGGTTTTCCTTGTCCAGATAGCTGACATTCATCCGGGGGTCAGC 4593 C 5206 ACCGTTTCTGCGGACTGGCTTTTCTACGGTTCCCAGTGACATTCATCCGGGGGTCAGC 5265 Db 4594 ACCGTTTCTGCGGACTGGCTTTCTACGGTTCCCTTTAGCAGCCTTGCGGGGTCGCTG 5265 C 5206 ACCGTTTCTGCGGACTGGCTTTCTACGGTTCCTTTAGCAGCCTTGCGCCTTGCGCCTTGCGCCTTGCGCCTTGCGCCTTGCGCCTTGCGCCCTTGCGCCTTGCGCCCTTGCGCCCTTGCGCCTTGCGCCCTTGCGCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCGCCCTTGCCCTTGCGCCCTTGCCCTTGCGCCCTTGCCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTT	SULT 2 260588 CUS CUS TRIATION SEQUENCE 16 from patent US 6489542 CESSION AR260588.1 GI:27311143 YWORDS UNKNOWN. UNKNOWN. UNKNOWN. UNCLASSIFIEG. FERENCE 1 (bases 1 to 8349) TERENCE 1 (bases 1 to 8349) TITLE Methods for transforming plants to	JOURNAL Patent: US 6489542-A 16 03-DEC-2002;	0y 2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG
3274 GATTTGCACTGCCGGTAGAACTCCCGCGAGGTCCTCAGCCTCAGCTGCAACCAA 3333 3946 CTCGCGAGGGGATCGAGCCTGGGGTGGGAGCTCCAGCTGGCTG	3574 GGGGAGGGGGATAAAGGAGGGAAAGCCATCAGCCCATTGGCGGCCAAGCTCTT 3633 4246 CAGCAATATCAGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGGCTCTT 3633 3634 CAGCAATATCAGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGC 3693 4306 CACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACATGATATCGGCAAGCAGGCT 4365	GTTCGGCTGGCGGGGGCCCCCCGATGCTCTTCGTCCAATCATCATCGATCG	4556 CCTTCCCGCTTCAGTGAGACACGTGGAGAAAGAACGCCGTGGTGCCA 4725 4054 CCTTCCCGCTTCAGTGAGACACGTGCGCAAGGAACGCCGTGGTGCCA 4113 4726 GCCACGATAGCCGCGCTGCTCCTGCAGTTCATTCAGGGCACCGGTCGTGCTCT 4785 4114 GCCACGATAGCCGCGCTGCTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGTCT 4173 4786 TGACAAAAAAAACCGGGCCCCTGCGCTGACGCGGACACGGCGCATCAGGCACCGGTCT 4173 4786 TGACAAAAAAAACCGGGCCCCTGCGCTGACGCGGAACACGGCGCATCAGGCGC 4233 4846 CGATTGTTGTTGTTGTTGTTCATCATCAGCGAAAACCGGCGCATAACCTCCCCCCAGGCGCAACACGGCGCAAAACGAACAGCGGCCCTGACGAAAACGAACCGGAAAACGAACAGCGGCCAAAACGGCCCAAACAGCGGCCAAAAAA

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126 AGCACCARGATACACCATTCCCGCCAAGCCCATTCACCAATTCACCAATTCCCGGTACC 7226 126 AGCACCAATTTCCCCATTCCCCATTCCCCCCAACCCGCCACCACCTCATTCCATTCC
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SYNBKURGS LOCUS SYNBKURGG SYNBKURGG LOCUS DEFINITION SOUTCE ACCESSION M17626 W17626 WIT 7626 WIT 1207845 WIT 1	AUTHORS Pridmore,R.D. TITLE New and versatile cloning vectors with kanamydin-resistance marker JOURNAL Gene 56 (2-3), 309-312 (1987) MEDLINE 88056335 PUBMED 3315864 COMMENT Original source text: Plasmid pBRNeo and pUC18 DNA. FEATURES Location/Qualifiers	7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.	/db_xref="G1:207846" //translation="MEQDGLHAGSPARWERLEGYDRAQQTIGCSDAAVFRLSAQGR PVLFVXTDLSGALNELQDEARLSMLATTGVPCAAVLDVVTEAGRDMLLLGEFVEQDL LSSHLAPPRKVSIYMADAWRLHTLDPEXTCPFDHQAKHRIERAFTRMEAGLYDQDDLDE EHQGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY QDIALATROIAEELGGEWADRFLVLYGTAAPDSGRIAFYRLLDEFF" BASE COUNT 584 a 724 c 769 g 584 t ORIGIN	Query Match 42.3%; Score 2233.4; DB 12; Length 2661; Best Local Similarity 93.4%; Pred. No. 0; Matches 2403; Conservative 0; Mismatches 26; Indels 144; Gaps 1; Qy 2711 GGTAATGATGGTGATATTCTGGTGAAATTGTTATCGGCTCACAATTCCACACA 2770 Db 2443 CGTAATCATGGTCATAGCTGTCAAATTGTTATCGCTCACAATTCCACACA 2384	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		######################################

ACCESSION 138499 Grade fragment. NERSION (198491.) GI:986977 KEYWORDS ccdB gene: cloning vector; kanamycin resistance. Cloning vector pKIL118 ALTHICALS sequences; vectors. REFERENCE (Loning vector pKIL118 ALTHICALS sequences; vectors. AUTHORS Bernard.P. JOURNAL Gene 152 (1), 159-160 (1995) ALTHICE (1), 159-160 (1995) FEATURES (1), 159-160 (1995) FEATURE	Query Match Best Local Similarity 93.4%; Pred. No. 0; Best Carrocarractoraractoraractoraractoractora
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Bernard, P.
New codB positive-selection cloning vectors with kanamycin chloramphenicol selectable markers
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                                                                                                                                                                                                                                                 26; Indels 146;
           /organism="his-3 integration vector pJHAM002"
/mol_type="genomic DNA"
/db_xref="taxon:220725"
                                                                               pJHAM001
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1.0597
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2598. .11373
/note="his-3 HindIII fragment"
6156. .6183
/note="multi-cloning sites"
12 a 2977 c 3096 g 2558 t
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Best Local Similarity 93.2%; Pred. No. 0;
Matches 2359; Conservative 0; Mismatches
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                                                                       1. .2597
/organism="his-3 integration vector pJHAM001"
/organism="his-3 integration vector pJHAM001"
/dol_type="genomic DNA"
/dol_txef="texcon:220724"
259E. .11403
/note="his-3 HindIII fragment"
/793. .7845
/note="multi-cloning sites"
4 a 3059 c 3033 g 2757 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2177.4;
Pred. No. 0;
0; Mismatches
/db_xref="taxon:220727"
/focus
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Best Local Similarity 93.2%;
Matches 2359; Conservative
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his-3 integration vector pUHAM004
artificial sequences; vectors.
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Lee,D.W., Haag,J.R. and Aramayo,R.
Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of
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in the amino acid-producing bacterium

Cloning vector pK19MECA2
artificial sequences; vectors.

I (bases 1 to 3210)
S Kirchner, O. and Tauch, A.
Tools for genetic engineering in the amino acid-producing bacteriuu Corymabacterium glutamicum
L Unpublished
E 2 (bases 1 to 3210)
S Kirchner, O. and Tauch, A.
Direct Submission
L Location/Qualifiers

SOURCE

AUTHORS TITLE

REFERENCE

TITLE JOURNAL

FEATURES

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JOURNAL
REFERENCE
AUTHORS
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CDS

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Best Local Similarity 86.7%;
Matches 2434; Conservative 2769 2829 3009 2889 2949 2970 2910 3069 BASE CC ORIGIN ò 임 ઠે 유 ठ 셤 8 g à 셤 ઠે g 8 8 circular SYN 23-MAR-2003 AY219859
Cloning vector pX19MECA2, complete sequence.
AY219859.1 GI:29164979

RESULT 10
AY219859/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

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Shuttle vector pEC-K19mob2
artificial sequences, vectors.

1 (bases 1 to 5695)
Kirchner,O. and Tauch,A.
Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
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/mol type="genomic DNA"

/db_xref="taxon:224992"

/note="Bscherichia coli-Corynebacterium glutamicum shuttle
                                                                        5178 CAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTC 5237
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PSTRELAGELGYSERRIQQYRKALGMEAKRGRYRANI
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| SDLETLVADLEELADELRARQRQEDAQ"
                             Chases I to 5695)
Kirchner, O. and Tauch, A.
Direct Submission
Submitted (22-JAN-2003) Department of Genetics, University of Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany Location/Qualifiers
                                                                                                                                                CGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
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Shuttle vector pEC-K19mob2, complete sequence.
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TITLE
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JOURNAL
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39.5%; Score 2088.4; DB 12; Length 5869; 86.7%; Pred. No. 0;	Matches 2434; Conservative 0; Mismatches 141; Indels 231; Gaps 3; Qy 2709 GACGTAATCATGGTCATAGGTCTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACA 2768	Qy 2769 CAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGGTGCCTAATGAGTGAG	Qy 2829 CACATTAATTGCGTTCAGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCGTCGTCGTGCCAGCT 2888 Dh E740 AACAMMANAMACCCTGTCACTMANACTCCTGTTTCCATTANACTCCTANAACTCCTCAAACCTTCAACAACTCCAACAACTCCAACAAC	2889 GCATTAATGAATCGGCCAACGCGGGGAGAGGGGGTTTGCGTATTGGGGCTCTTCCGC 2 5689 GCATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTTGCGTATTGGGCTCTTCCGC 5689 GCATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGTATTGGGCTCTTTCCGC 5	Qy 2949 TICCTGGCTGACTGACTGGCTCGGTCGTTCGGCTGCGGCGAGGGTATCAGCTCA 3008 Db 5629 TICCTGGCTCACTGACTCGCTCGGTCGTTCGGCTGCGGCGGCGGGGGGGG	Qy 3009 CTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTG 3068 	OY 3069 AGCAAAAGGCCAGCAAAAAGGCCAGGAAAAAAGGCCGCGTTGCTGGCGTTTTTCCA 3128	OY 3129 TAGGCTCCGCCCCTGACGACGTCACAAAAATCGACGCTCAAGTCAGGGGGGGG	0y 3189 CCCGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC 3248	A 3249 TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC 3308	Oy 3309 GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCCAAGCT 3368	Ay 3369 GGGCTGTGTGCACGCCCGGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCG 3428	QY 3429 TCTTGAGTCCAACACGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAACAG 3488	Qy 3489 GATTAGCAGAGGGAGGTATGTAGGGGGGGGCTGCTGAAGTAGTGGTGGCCTAACTA 3548	OY 3549 CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG 3608	OY 3609 AAAAAGAGTIGGTAGCTCTTGATCCGCCAAACAACCACCGCTGGTAGCGGTGGTTTTTT 3668	Qy 3669 TGTTTGCAAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTT 3728
VERSION AY219861.1 GI:29164983 KEYWORDS SOURCE Shuttle vector pEC-K19MECA2 ORGANISM Shuttle vector pEC-K19MECA2	arthicial sequences; vectors. 1 (bases 1 to 5869) AUTHORS Kirchner,O. and Tauch,A. TITLE Tools for genetic engineering in the amino acid-producing bacterium COTYPREBACTERIUM glutamicum	Z (bases 1 to 5869) Kirchner, O. and Tauch, A. Direct Submission	Bielefeld Ce	(A)	gene 5742037 /gene="repA" CDS 5742037	/gane="replation protein" /note="replation protein" /codon_start=1 /ransl_table=11 /ransl_table=11	/prodecin_id="AA065228.1" /brotein_id="AA065228.1" /db_xref="GI:29164984" /translation="MTLADPQIPTVTASAWKLSADLFDTHPEANRCGSRGWTAEDRREL ***********************************	IMITORIES VESTATURAS PERMITANOS MEDICETETANOS MEDITACOS MEDITANOS MEDITACOS MEDITACISMOS MEDITACOS MEDITACOS MEDITACOS MEDITACOS MEDITACOS MEDITACISMOS MEDITACOS MEDI			/note="positive effector of replication" /codon_start=1 /transl_table=11 /product="Per" /product="Per"	/db_xref="G1:29164985" /translation="MDLSDVALESDALDAAVDLKTVIGFFRALDTTDAPASRAMASAA SDLETLYNDLEELADELERARQRQEDAQ" 3414 4208	/gene="aph(3')-IIa" 34144208 /gene="aph(3')-IIa"	/note="aminoglycoside phosphotransferase" /codon_start=1 /transl_table=11 /product="Aph(3')-11a"	/ptotenii ida=Amboszau.i. /db_xref="Gi:29164986" /translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR /UFVKTDLSGALINELODBAARLSWIATTGVPCAAYLDVVTAGARDWILGEVPGODL regut paparkethanamader in nammentenden et bea enswerket income na	ERGGLAPALLARAKPANANILIAN OFFINANILIAN OFFINANILIAN INMANANILANINANIN	/note="RP4-mob region" rep_origin 5454. 5456 /note="oriv" BASE COUNT 1325 a 1669 c 1683 g 1192 t

4978 GARTCAGCCATGATTGATTCTCGGCAGGAGCAAGGTGACAGGAGATCCTCC 4637 4538 CCCGGCACATTGGCCCAATACAGCAGCAGGAGGAGATCCTCC 4637 4538 CCCGGCACATTGGCCCAATACAGCCAGTTCCCGTTCAGTGACAGGAGATCCTCC 3710 4539 CCCGGCACATTGGCCCAATACAGCCCAATACCGGCTTCAGTGACACAGCAGATTCTCCTC 4549 GCTTGGCCAAGGACCCCCAATACAGCCCAATACCGGCTCCTCTCTCT	RESULT 13 AF445080/c LOCUS AF445080 Cloning vector pEC-K18mob2, complete sequence. DEFINITION AF45080. VERNION AF45080. AF45080. AF45080. AF45080. AF45080. AF45080. AF45080. AF45080. AF45080.1 GI:17386067 KEYWORDS Cloning vector pEC-K18mob2 Cloning vector pEC-K18mob2 AF45080. AF445080. AF445080
TICTACGGGGTCTGACGTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGG 1788	### ##################################

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TITCGCACGATATACAGGATITITGCCAAAGGGTTCGTGTAGACTITCCTTGGTGTATCCA
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/noce="RP4 mob region"
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/noce="oriv of Escherichia coli"
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misc_feature 17631861 /note="RP4-mob region" rep_origin 26242626 /note="ority"	665 a 841 c 39.3%;	Best Local Similarity 86.7%; Pred. No. 0; Matches 2423; Conservative 0; Mismatches 140; Indels 231; Gaps 3; 272; GTGATAGCTGTTTCCTGTGAAATTGTTATCGGCTCACAATTCCACACAACATACGAGC 2780	7 GICAIAGCTGTTTCCTGTGTGAAATTGTTATCGCTCACAATTCCACACATACGAGC 7 CCCAAACCAAAAAAATTGTTATCGCTCACACATACCACACAATTGC	CGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG	OY 2841 GTTGCGCTCACTGCCGGTTTCCAGTCGGGAAACCTGTCGTGCCAGTGCATTAATGAAT 2900 Db 2907 GTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAAT 2848	2901	2961 TGACTCGGTGCGGTCGGTCGGCGGGGGGGGGTATCAGCTCACTCA	3021 AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 	OY 3081 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGCGCGTTTTTTCCATAGGCTCGGCCC 3140 Db 2667 GCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGCCGCTTTTTCCATAGGCTCCGCCC 2608	OY 3141 CCCTGAGGATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGAT 3200 Db 2607 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 2548	Qy 3201 ATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTCGTGGGGCTCTCCTGTTCCGACCCT 3260 Db 2547 ATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCTCGTGCGCTCTCCTGTTCCGACCCT 2488	OY 3261 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCADAG 3320 Db 2487 GCCGCTTACCGGATACCTGCCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG 2428	OY 3321 CTCACGCTGTAGGTATCTCAGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTCCA 3380 DD 2427 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGCA 2368	OY 3381 CGAACCCCGGTTCAGCCGGCTGCGCCTTATCGGGTACTATCGTCTTGAGTCCAA 3440 Db C3867 CGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCGGGTACTTGAGTCCAA 2308	OY 3441 CCCGGTAAGACACGACTTATCGCCACTGGCAGCACCACTGGTAACAGGATTAGCAGAGC 350 Db 2307 CCCGGTAAGACACTTATCGCCACTGGCAGCACCACTGGTAACAGGATTAGCAGAGC 224	9y 3501 GAGGTATGTAGGGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG 356	QY 3561 AAGAACAGTATTTGGTATCTGGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGG 3620 Db 2187 AAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGG 2128	Qy 3621 TAGCTCTTGATCCGGCAAACAACGACGCTGGTAGCGGTGGTTTTTTTT

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Cloning vector pKl8PolyF2
artificial sequences; vectors.

1 (bases 1 to 3053)
Tauch,A., Kirchner,O., Loffler,B., Gotker,S., Puhler,A. and Kalinowski,J.
Efficient electrotransformation of Corynebacterium diphtheriae with a mini-replicon derived from the Corynebacterium glutamicum plasmid
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                                                                                                                                                                                                                                                                                                                                      CCTGTCTTCTTGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGCAAGAAGCC
                                                                                                                                                  ACGCCCCTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCCTGCAGGTTCAGGGCA
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AY222811
AY222811.1 GI:29169334
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2 (bases 1 to 3053)
Tauch, A., Kirchner, O., Loffler, B., Gotker, S., Puhler, A. and
Kalinowski, J.
Direct Submission
Submitted (12-JAN-2003) Department of Genetics, University of
Bielefeld, Universitatsstrasse 25, Bielefeld D-33615, Germany
Location/Qualifiers
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Pred. No. 0;
0; Mismatches 140;
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| forganism="Cloning vector pXl
| (mol_type="genomic DNA"
| db_xref="taxon:224892"
| Lab_host="Escherichia coli"
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345 TICATCCGGGGTCAGCACTTICIGCGGACTGGCTTTCTACGTGTCCGCTTCCTTTAG 286 g

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Search completed: February 15, 2004, 16:21:29 Job time : 18649 secs

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February 15, 2004, 05:44:19; Search time 1245 Seconds (without alignments) 11454.724 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                      2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           - nucleic search, using sw model
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5283
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Description	Expression vector	pMON30464 plasmid.	Hybrid NAMK.6 (ter	Synthetic DNA plas	GENSA 981, a monom	Nucleotide sequenc	Plasmid VLSNO2 DNA	Nucleotide sequenc
ID	ABK10062	AAA15565	AAV29673	AAX52020				
DB	24	21	19	20	19	22	13	24
% Query Match Length DB ID	5283	8349	6136	4800	5594	5285	6561	2192
% Query Match	100.0	42.4	38.2	33.9	31.3	30.9	30.6	30.4
Score	5283	2240	2017.2	1793.4	1652.4	1634.4	1618.2	1603.8
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Coleman TA;

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ABQ78293	42	2	AAV50427	AAV40795	AAX88055	AAZ40417	AAF30342	AAX84027	AAH24427	AAV33626	AAD42469	AAZ25355	AAZ25354	AAZ25353	AA225351	AAA07773	AAA07778	ABZ24716	AAA07779	AAZ40023	AAA07847	AAA07845	AAA07846	AA168460	AAD10015	AAL47954	ACC44640	AAA50945	AAA48561	AAA48562		AAA07772	AAA07777	G	AAA50946	AAA50947
54	5	13	19	19	20	20	22	20	22	19	24	20	20	20	20	21	21	25	21	21	21	21	21	22	22	24	25	21	21	21	25	21	21	25	21	21
3534	3599	3599	3600	3600	5707	2966	4665	5068	4517	4518	4886	5031	5054	5130	5168	5619	5627	5775	6121	6139	7655	8140	11842	4055	4653	4692	4692	4695	4700	4700	4727	4729	4735	4740	4821	4821
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σ,	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1; chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a; allergic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferative disorder; viral infection; bacterial infection; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; gene therapy. Expression vector construct pVGI.1 containing VEGF-2 insert. 뗦 ABK10062 standard; DNA; 5283 (HUMA-) HUMAN GENOME SCI INC 04-AUG-2000; 2000US-223276P. 03-AUG-2001; 2001WO-US24658. (first entry) WO200211769-A1. 21-MAY-2002 14-FEB-2002. Synthetic. ABK10062;

WPI; 2002-217153/27 conditions

Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischaemia or myocardial ischaemia, autoimmune disorders and allergic

Disclosure; Fig 31; 241pp; English

The invention relates to an isolated nucleic acid comprising pVGI.1 factors construct containing the vasualar endothelial growth factor 2 (VGF-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell with the DNA and for treating a patient having chronic limb ischaemia or myocardial ischaemia, or a disease or disorder selected from autoimmune disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. conditions, desase), diseases), diseases), diseases (e.g. cardiomyopathy), arthythata, heart valve diseases, aneurymms, arterial occlusive disorders and embolism. This sequence represents the pVGI.1 expression vector containing the VEGF-2

Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 other;

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540 540 900 900 120 120 GGGATTICCAAGICTCCACCCCACTGACGICAAIGGGAGITIGITITIGGCACCAAAAICA 180 180 240 ACGAGACTITICCAAAATGTGGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240 306 241 AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTG 300 CATGCCGATTGGTGGGAGTAAGGTGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAG 360 GCAACAGACGGGTCTAACACGGATTGGACGAACCACTGAATTCCGCATTGCAGATATT 420 gcaacacacacactraacacacarracacaacaaccacraarrecacarracaaaararr 420 480 GTATITIAAGIGCCCAGCICGAIACAAIAAACGCCAITIGACCAIICACCACAITGGIGIG 480 9 9 CACCTGGGTTGGGATCGATCATGCACTCGCTGGGCTTCTTCTTCTGTGGCGTGTTCT GAGTCCGGACTCGGACGCGGAGCCCGACGCGGGGGCGACGCCACGGCTTATGCA GTATTTAAGTGCCCAGCTCGATACAATAAACGCCATTTGACCATTCACCACTTGGTGTG caccrederressarcearcearcareaciescressecricircricrerereserrer CTGCTCGCCGCTGCGCTCCCCGGGTCCTCGCGAGGCGCCCCGCCGCCGCCGCCGCCGCCGCCTTC GAGTCCGGACTCGACCTCTCGGACGCGGACGCGGGTGAGGCCACGGCTTATGCA TACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACG ACGAGACTITICCAAAATGICGIAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAAAAAAGCACCGTG ICCTACTIGGCAGIACAICTACGIAITAGICAICGCIAI Gaps 100.0%; Score 5283; DB 24; Length 5283; .larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; 1 AAGCTTGACCTTATGCGACTT Best Local Similarity Matches 5283; Conserv 601 541 361 481 61 181 181 241 301 301 361 421 421 481 Query Match 61 121 121

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à	661	AGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGTAGAAGTCATGACTGTA 720
Db	661	AGCAAAGATCTGGAAGGAGTACGGTCTGTGTCCAGTGTAGATGAAACTCATGACTGTA 720
e Š	721	CICTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACAT 780
Dp	721	CICIACCCAGAATATIGGAAAATGTACAAGTGTCAGCTAAGGAAAGGA
ò	781	781 AACAGAGAACGCGAACCTCAACTCAAGACAGAGAGACTATAAATTTGCTGCAGCA 840
g Q	787	AACAGAGAGCAGCCAACCTCAAGTCAAGAACAGAAGACIAIAAAA111GCTGCAGCAA GTG
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Š	1261	GGAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCA 132
.qa	1261	ATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCA 1320
à	1321	_
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Š	1561	CTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAA 1620
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Š		81 AAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTGT
qq	1683	. AAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGTGTGTGT

	15565 AAA15565 standard; AAA15565; 28-JUL-2000 (first pMON30464 plasmid. Transgenic plant; ilepidopteran; bipte plasid targeting pe Synthetic. WO200026371-A1. 11-MAY-2000. 04-NOV-1999; 99W(04-NOV-1999; 99W(WPI; 2000-376130/32. X WPI; 2000-376130/32. Y New method of expressing insecticidal proteins in plants transformed with a Bacillus thuringlensis delta-endotoxin encoding gene resulting in effective control of susceptible target pests X Example 1; Page 96-99; 104pp; English. C proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran controlled which larvae. An insect-resistant transgenic plant has been constructed which contains the delta-endotoxin genes into plant cells and for cused to transfer delta-endotoxin genes into plant cells and for subsequent high expression of the cry2Ab gene. Protection may be attained against insects such as ostrina spp., Diatraea spp., Helicoverpa spp., C and spodoptera spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia spp., in Glycine max; and Scirophaga incertulas in Oryza corp. Epinotia comprising an anino-terminal plastid transit peptide (zmSSU PTP) coverinc Comprising to the delta-endotoxin. The fusion protein functions to covaliently linked to the delta-endotoxin the subcellular organelle or compartment.
3901 TAGAACTCCGCGGGGTCCTCCAGCCAGCAGCAGCTGAACCAACTCGCGGAGGGATCG 3960 3961 AGCCCGGGGTGGGCAAGAACTCCAGCATCAGCCGCGCGCG	TAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCCGGCCGCCACAGTCGATGATC TAGCCAACGCTATGTCCTGATAGCGGTCCGCCACCCCCGCCGCCCACAGTCGATGATC CAGAAAAGCGGCCATTTTCCACCATGATATCGGCAACCCGGCCGCCACAGTCGATGATC CAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGA CGGAAAAGCGGCCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGA CGAGAAAAGCGGCCCATTTCCACCATGATATTCGGCAAGCAGCACGCCATGGGTCACGA CGAGAACCTCGCCCTCACCACGCGCCTTGAACCTTGACCTGGCCATGGGCTCCCATGGGTCACGA CGAGATCCTCGCCCTCACCACGCGCCTTGAACCTTCGCCATGGCCATGGCCATGGCCATGGCCATGGCCATGGCCATGCCCTGATCCTCACCACGCAACCGCAACCACGCGCATCCCTGATCCTCCTGATCCTCGCTTCGCTTCGCTTGATCCTGATCGCCAAGCCGCATCCATC	4621 ATGACAGGAGATCCTGGCCGGGCCAATAGCAGGTCCCTTTCCGCTTCCGGTTCAG 4680 4681 TGACAACGTCGAGCACCTGCGCAATAGCCGCC 4740 4681 TGACAACGTCGAGCACAGGAACGCCCGTCGTGGCCACCACAATAGCCGC 4740 4741 CTGCCTCGTCCTGCTCATCAGGCCACCGACACGCCCACCACAAAAGAACCG 4740 4741 CTGCCTCGTCCTGCATTCATTCAGGCCACCGACAGGTCGGTC

	267 AGCACARGAGAAGCGGTCACCCATTCGCCCCAAGCTCTTCAGCATTTCHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
6 4 6 4 6 4 6 4 6 4 6 4 6 6 6 6 6 6 6 6	2 4 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5
Sequence 8349 BP; 1959 A; 2355 C; 2088 G; 1947 T; 0 other; Query Match Best Local Similarity 93.4%; Score 2240; DB 21; Length 8349; Best Local Similarity 93.4%; Pred. No. 0; Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 2706 CTAGACGTAATCATGGTCATTCCTGTGTGAAATTGTTATCGGTCACAATTCC 5911 CTTGGCGTAATCATGGTCATTACCTGTGTGAAATTGTTATCGGTCACAATTCC 7765 ACACATACACATACAGCAGAAAAGGTCAAAAGGTGAAAAGTGTAAAAGTGTAAAAATTGTTATCGGTCACAATTCC 7765 ACACAATACACATACAGGAACATAAAAGTGTAAAAGTGTAAAAAATTGTTATCGGTCACAATTCC 7765 ACACAATAATTGGCGTAGACATAAAAGTGTAAAAGTGTAAAAAATTGTTATCGGTCACAATTCCTGTGTGCAAATTCC 7767 ACACAATAATTGCGTTGCGGAAAAAAGTGTAAAAAGTGTAAAAAAAA	3126 CCATAGGCTCCGCCCCCTGACGACATCACAAAATCGACGCTCAAGTGGGG 3185 6331 CCATAGGCTCCGCCCCCCTGACGACATCACAAAATCGACGCTCAAGTGGGGG 6390 3186 AAACCCGACAGCCTGCCGCCCCTGACGATTCCCCCTGGAAGTCCGCTGGGGCC 6390 3246 TCCTGTTCCGACCCTGCCGCTAAAAGATACCAGGATTCCCCCTGGAAGCTCCTCCGTGGGCTC 6450 3246 TCCTGTTCCGACCTGCCGCTAAAAGATACCAGGATTCCCCCTTGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTCTTCGGGAAGCTTTCGGGAAGCTCTTCGGGAAGCTTTCGGGAAGCTCTTCGGGAAGCTTTCGGGAAGCTTTCGGAAGCTTTCGGGAAGCTTTCGGGAAGCTTTCGGGAAGCTTTCGGGAAGCTTTCGGGAAGCTTTCGGAAGCTTTCGGAAGCTTTCGGAAGCTTCGGTTAAGTTAGCTCGGTAAGTTCGTTC

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               CCTGCGCTGACACACCGGCGCCATCACAGCCGCGATTGTCTTGTTGTGCCCAG 7926
                                                                                                                  TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCAT 8046
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                                                                                                                                                                                                                                                                                                                                                                        8287 TICTACGIGITICCGCTTCCTTTAGCAGCCCTTGCGCCCCTGAGTGCTTGCGCAGCGTG 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion construct pNAMK6.1. This is an enzyme hybrid which can be used for the liquefaction of starch. The enzyme hybrids contain amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Starch, liquefaction, sweetener; enzyme hybrid; endoglucanase; enzyme; cellulose binding domain; CBD; starch processing; alpha-amylase; saccharification; Termamyl-linker-CBD fusion; ss.
CCCTGCGCTGACAGCCGGAACACGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG
                                                TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT
                                                                                                 TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCAT
                                                                                                                                                   CAGATCCTTGGCGGCCAAGAAAGCCATCCAGTTTACTTTTGCAGGCTTCCCAACCTTACCA
                                                                                                                                                                         8047 CAGATCCTTGGCGGCAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA
                                                                                                                                                                                                   GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTTGCTGTCCATAAAACCGCCCAGTCTAGC
                                                                                                                                                                                                                             8107 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTTGCTGTCCATAAAACCGCCCAGTCTAGC
                                                                     7927 TCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGT
                                                                                                                                                                                                                                                      TATCGCCATGTAAGCCCACTGCTACCTGCTTTCTCTTTTGCGCTTGCGTTTTCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biquefaction of starch for, e.g. production of sweeteners -
comprises use of enzyme hybrids including cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid NAMK.6 (termamyl-linker-CBDEGV) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bjornvad M, Pedersen S, Schulein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Pages 65-67; 83pp; English.
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Humicola insolens.
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of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is selected from the Bacillus or cellulomonas endoglucanase, C. xylanase A or the Humicola insolens BdV sequence. The starch is liquefied by treating, in aqueous medium, with such an enzyme hybrid. A recombinant expression vector comprising a construct containing isolated DNA encoding enzyme hybrids with amylolytic activity, promoter and stop signals can be used to transform host cells for the production of the recombinant enzyme hybrids. The enzyme hybrids are useful in industrial starch processing affinity for substrate and increased activity, resulting in at least 1 of reduced calcium ion dependence, reduced formation of Maillard reaction products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.2%; Score 2017.2; DB 19; Length 6136; Best Local Similarity 91.8%; Pred. No. 1.1e-303; Matches 2203; Conservative 0; Mismatches 53; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            saccharification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3604
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3664 ITITITIGITIGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG 3723

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AGCCGATTGTCTGTGCCC 4863
                                                        AACCTGCGTGCAATCCATCTT 4923
                                                                                                                                         IGCAGGGCTTCCCAACCTTAC 5043
                                                                                                                                                                                                                                                                                                       CTGAGTGCTTGCGGCAGCGTG 5283
                                                                                                                                                                                                                                                               AGCACCGTTTCTGCGGACTGG 5223
                                                                                                   CAGATCTTGATCCCCTGCGCC 4983
                                                                                                              retriegectiegetitiege 5163
                                                                                                                                                                                                                                      CTTGACAAAAGAACCGGGC 2606
                                                                                                                                                                                 FCCATAAACCGCCCAGTCTA 5103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid sequence,
s. Within the sequence
A and B components of
ons of pUC19 including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ferase; promoter;
ynthesis;
tide; ss.
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the origin of replication and replication stability sequences, and the promoter and coding sequence for the knammycin/hosomycin phosphotransferase. The plasmid was synthesised form 192 50-mers (see phosphotransferase. The plasmid was synthesised form 192 50-mers (see AAX52021-12) to demonstrate the method of the invention. The specification describes a method for the synthesis of replication competent double-stranded polynucleotides. The method comprises generating a first set of oligomucleotides corresponding to the plus strand and a second set corresponding to the minus strand and ameasing. The method can be used for preparing polynucleotides encoding sequences involved in a biochemical pathway. In particular, they can be used to produce polynucleotides encoding enzymes, e.g. hexofinase, phosphotexose isomerase, phosphotetokides encoding enzymes, e.g. hexofinase, phosphotetokides encoding enzymes, e.g. hexofinase, phosphotetokides enclase or pyruvate kinase, phosphotetoke mutase, enclase or pyruvate kinase. They can artificial genetic systems.

Sequence 4800 BP; 1345 A; 1032 C; 1163 G; 1260 T; 0 other;

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3127 CATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA 3186 4800 CATAGGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA 4741 3187 AACCCGACAGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT 3246 4740 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGTCT 4681 3247 CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG 3306 3307 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 3366 CTGGGCTGTGTGCACGAACCCCCCGGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT 3426 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAAC 3486 3487 AGGATTAGCAGAGGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 3546 4440 AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGTGGCTAAC 4381 TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 3606 3607 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTT 3666 GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT 4261 TITGITTGCAAGCAGCAGAATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC 3726 3727 ITITCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATG 3786 4200 riticiacososrcroacosrcadosaacosaaacrcacorraagosarrirogroar 4142 3787 AGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATGG 3846 3847 ATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAAC 3906 4680 CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG 4621 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG 4561 4560 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT 4501 cencingaenceaacecenaadacaceacinarececacidecageaceaceacidarae 4441 4380 TACGGCTACACTAGAAGACAGTATTTAGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC 4321 4260 Trigiringcaagcagcagarracgcgcagaaaaaaagarcrcaagaagarccrrigarc 4201 1; Indels 176; Gaps 33.9%; Score 1793.4; DB 20; Length 4800; ilarity 91.8%; Pred. No. 4.9e-269; Conservative 0; Mismatches 1; Indels 176; G Local Similarity Best Local Sim. Matches 1980; 4620 3427 4500 4320 3667 3547 3367 Query Match

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q	4141	4142
ò	3907	TCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCCG 3966
g	4141	2CCG 4
ð	3967	
g	4136	addigadaacticcadcardadarcccccccccadaacaarcarccadccc
8 8	4027	CGGABAACGATTCCGBAGCCCAACCTTTCATAGAAGGGGGGGGGG
e :	4076	CGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGGGGGGG
6 6	0 ~	GATGGCAGGCTTGGCTCGCTCGGTCGTTTTCGAACCCCAGAGTCCGCTCAGAAGA 395
à	1.4	ACTCGTCAAGAGGGGATAGAAGGCGATGCGCGAATCGGGAGGGGGGGG
Q	ທັ	ACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAAGCGGCGATACCGTAAA 389
දි දි	420 <i>7</i> 3896	GACGAGGAAGCGGTCAGCCCATTCGCCGCCAGCTCTTCAGCAATATCAGGGGTAGCCA 42 GCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCA 38
ò	4267	TANGACCIGATAGCGGTCCGCCACCACCCGGCCACACACTGAATCCAGAAA 432
g	3836	ACGCTATGTCCTGATAGCGGTCCGCCACCCCAGCCGGCCACCAGTCGATGAATCCAGAAA 37
à á	4327	AGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGAT 438
3 8	- 00	COTOGOCATICAGACATACACACATTAAAACATAAAAAAAAAAATTAAAATTAAAAAA
· 名	, , ,	CTCGCCGTCGGGCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCT 365
à	4447	GATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTC 450
Q	3656	GAIGCTCTTCGTCCAGATCATCCTGATCGACGACCGGCTTCCATCCGAGTACGTGCTC 3
8	20,	GCTCGATGCGATGTTTCGCTTGGTGGAGTGGGCAGGTAGCCGGATCAAGCGTATGCA 45
台	9	CGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCA 353
8 8	4567	GCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACA 4626
ò	4627	GGAGATCCTGCCCGGCACTTCGCCCAATAGCAGCCCAGTCCCTTCCCGCTTCAGTGACAA 4686
ą	3476	GGAGATCTIGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGGCTTCAGTGACAA 341
8 8	4687	CGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCACCACGATAGCCGCGCTGCCT 4746
3	1	
8 3	4747	GOCCHGGATTCATTCAGGGACCGGACAGGTCGGTCTTGACAAAAAACCGGGCCCC 4806
ò	4807	CCTGCGCTGACAGCGGGAATCAGGGGGGCATCAGAGCCGATTGTCTGTTGTGCCCAGT 486
മ്	3296	CCTGCGCTGACCGGGAACACGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCA
ờ		CA .
q	3236	CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAAACCTGCGTGCAATCCATCTTGTT 317
ઠે	Ò	CAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATC 498
e G	3176	caarcareceaaacearccicarcciercicitearcaearcrigarecearc

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The invention provides a novel method for directing self-assembly of a gene having three or more fragments in a directionally and spatially cordered fashion to produce a gene or a gene vector. The method involves usage of primers, containing class IIS restriction endonuclease recognition sites, for isolation of these fragments. As described in the disclosure, the method may also use a vector for the incorporation and screening of endogenous mouse promoter elements for the identification of cell specific promoters. In the example given, plasmids pBx.CMV (AAV33626), pVLMB (AAV33623) and pVLOVDGH-900 (AAV33621) were used as templates from which six fragments were amplified. Each of the fragments contained different requiatory sequences. The six PCR fragments were designed to self-assemble into a retro-vector using the method of the invention. The present sequence, designated as GRNSA 991, represents the monomeric DNA sequence of the six ligated fragments. In general, the method is claimed to be useful for
4987 AGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAG 5046
                             .
3116 AGATCCTTGGCGGCAAAGAAAGCCATCCAGTTTACTTTGCAGGCTTCCCAACCTTACCAG 3057
                                                                                      AGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT 5106
                                                                                                                                   3056 AGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT 2997
                                                                                                                                                                             5107 ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTTGCGCTTGCGTTTTCCCTTG 5166
                                                                                                                                                                                                                                                                      TCCAGATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTT 5226
                                                                                                                                                                                                                       2996 ArcaccardraAsacccacraccaaccraccracriricreringseacririccering 2937
                                                                                                                                                                                                                                                                                                                5227 TCTACGRGTTCCGCTTCCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG 5283
                                                                                                                                                                                                                                                                                                                                                                                                         2876 rozacenerrocecrirorrizaceaececrirececereaerecriececeaecere 2820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for assembling gene or gene vector - comprises use of primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class IIS restriction endonuclease recognition site; endogenous mouse promoter element; tissue-specific gene expression; hormone-specific gene expression; ss; developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENSA 981, a monomeric DNA sequence produced by the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Pages 107-110; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV33629 standard; DNA; 5594 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NATU-) NATURE TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu G, Zink MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0070910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US03918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-495399/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9838326-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hodgson CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                      5167
                                                                                         5047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV33629
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ID AAV336
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5472
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                                                                                                                                                                                                                                                                              3107 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGAC 3166
                                                                                                                                                                                                                                                                                                                              5591 cescerrecrescerrirrecarasserrececececereaceaecareacaaaaaresae 5532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5411 TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGG 5352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3407 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC 3466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCCGGTGCTACAGAGT 3526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC 3586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5171 TCTTGAAGTGGTGGCCTAACTACGGCTACACAAAGGACAGTATTTGGTATCTGCGCTC 5112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCA 3646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3647 CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCCCAGAAAAAAAGGAT 3706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5051 CCGCTGGTAGCGGTGGTTTTTTTTTTGTTTGCAAGCAGCAGATTACTGGCGCCCCGAGTGAGG 4992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3707 CTCAAGAACCTTTGATCTTTTCTACGGGTCTGACGCTC-----AGTGGAACG 3757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3758 AAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCGTCGACCAAAGCGGCCATCGTGC 3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4931 AACTGATTGGTTAGTTCAAATAAGGCACAGGGTCATTTCAGGTCCTTGGGGGCACCCTGGA 4872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3818 CTC------CCCACTCCTGCAGTTCGGGGGCATGCGCGGGTTAGCCGCTG 3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4871 AACATCTGATGGTTCTCTAGAAACTGCTGAGGGCTGGACCGCATCTGGGGACCATCTGTT 4812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3865 CIGGITICCIGGAIGCCGACGGAITIGC-----ACTGCCGGIAGAACTCCGCGAG 3914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4811 CTTGGCCCTGAGCCGGGCAGGAACTGCTTACCACAGATATCCTGTTTGGCCCCATATTCA 4752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGTCCAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGGATCGAGCCCGGGGGTGGGGC 3974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3975 GAAGAACTCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGGCGTCCCGGGAAAAC 4034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4691 TITGGCCCATATICAGCTGTTCCATCTGTTCCTGACCTTGATCTGAACTTCTCTATICTC 4632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4991 GGTTGTGGGCTCTTTTATTGAGCTCGGGGAGCAGAACGCGCGCAACAGAAGCGAGAAGCG 4932
isolating and identifying regulatory sequences from a cell, including those for enhanced biological activity, or tissue-specific, hormone-specific or developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGCICCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3167 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                             5531 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5291 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGCACTTATCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        renadercernecaachedecrenenacaceaceaacecececancadeceaaceen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5231 TeechecaeccacTeeTaacaecaTTaGCaeaeCGaeGTaTGTaGGCGGTGCTACAGAGT
                                                                                                                                                                                                                     67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5471 GAAGCTCCCTCGTCCTCTCTTCCGACCCTGCCGCTTACCGGATACCTGTCGCCT
                                                                                                                                                                     DB 19; Length 5594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICICCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT
                                                                                                            Seguence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 other;
                                                                                                                                                               Query Match
31.3%; Score 1652.4; DB 19; Lengt
Best Local Similarity 85.4%; Pred. No. 3.2e-247;
Matches 1916; Conservative 0; Mismatches 261; Indels
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ò	4035 GATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCTGAAATCTCG 4085	Qy 5080 CTGT Db 3551 CTGT	CTGTCCATAAAA CTGTCCATAAAA
Q Q	4631 AGTTATGTATTTTCCATGCCTTGCAAAATGGCGTTACTTAAGCTAGCT	Oy 5140 TICE	TTCTCTTTGCGC
ç ç	4086	Db 3491 TTCT	
8 8	TCGAACCCGGATCCCGCTCAGAAGAACTCGTCATGAGAAGGCGATGCGCT 4	OY 5200 GTCA Db 3431 GTCA	GTCAGCACCGTI
qq	4511 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT 4452	5260 6	CCCTGAGTGCT
, ₽ ₽	4180 GCGAATCGGGAGCGGGATACCGTAAAGCACGAGGAGGGGTCAGCCCATTCGCCGCGAA 4239	3371	GCCCTGAGTGCT
% eg	4240 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCA 4299	RESULT 6 AAH74865/c ID AAH74865 standard;	ndard; DN
දු දු	4300 GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 4359 	XX AC AAH74865; XX DT 29-OCT-2001	(first e
δ	4360 AGGCATGGCCATGGGTCACGAGATCCTCGCCGTCGGCGCCTTGAGCCTGG 4419	Nucleotide	sednence o
D.P	4271 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCCTTGGCCTGG 4212	Rolling	circle replic
ry Sp.	4420 CGAACAGTTCGGCTGGCGGGGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA 4479	Syntheti Porcine	circovirus.
<u>ک</u> ج	4480 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG 4539 [1][FN W0200161024-A2 XX PD 23-AUG-2001	A2.
ें	GGCAGGTAGCCGGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGGATACTT	15-FEB-2001;	2001WO-L
qq	4091 GGCAGGTAGCCGGATCAAGCGTATGCACCGCGCATTGCATCAGCCATGATGCATTACTT 4032	16-FEB-2000;	2000US-(
& 8	4600 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA 4659 4031 TCTCGGCAGGAGCAAGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA 3972	PA (LARG-) LARGE XX PI Palmer KE, Po	Pogue GP
δδ	GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAAGGAACGCCCGTCG		
ç C	gccagtcccttccccttcagtgacaacgtcgagcacagcgcgcgaaggaacgcccgtcg		eotide ca iscovery
& g	4720 TGGCCAGGATAGCCGCGCTGCTGGTGCTGGAGTTCATTCA	PT that are cis on the proper protein of interest XX	on the present
ò	CGGTCTTGACAAAAAAAAACCGGGGCGCCCTGACAGCAGCGGGAACACGGGGATCAG		ig 5; 61 <u>1</u>
연	3851 CGGTCTTGACAAAAAGAACCGGGGCCCCCTGCGCTGACGCGGAACACGGGGGCATCAG 3792	CC The specification des CC circle replication (N	ation de cation (1 Rep gene
ठे व	AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCAAAGCGGCCG		eotide si de, an oj
ga .	AGCAGCCGATTGTCTGTTGTCCCAGTCATAGCCTCTCCCACCCA		where
è 8	4900 AGARACCIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		and Nancy y of the
Š	4960 GAICAGAICCIGACCCAGCCCATCAGAICCTIGGCGGCAAGAAAGCCAICCAGTIA 5019	CC down-regulating a ger CC or even eliminating (ing a ger inating (
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දු දු	5020 CTTTGCAGGGTTTGCAACGTTACCAAGGGGGCCCCCAGGGAATGCGGTTG 5079 3611 CTTTGCAGGGCTTCCCAACGTTACCAGAGGCGCCCCAGCTGGCAATTCGGGTTGTTG 3552	CC or cells), and in who cc a construct comprisit CC pcv Rep gene under the	nd in who comprisi
			tive coa

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5080 CIGICCAIAAAACCGCCCAGICTAGCIAICGCCAIGTAAGCCCACTGCAAGCTACCTGCT 5139
151 CIGICCAIAAAACCGCCCAGTCIAGCTAICGCCAIGTAAGCCCACTGCAAGCTACCGCT 3492
                                                                                                                                                                                                      CGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGC 5259
                                                                                                                                                                                                                                    GCGCTTGCCTTTTCCCTTGTCCAGATAGCCCCAGTAGCTGACATTCATCCGGG 5199
                                                                                                                                     GGCCTTGCCTTGTCCCAAAAACCCCAGTAGCTGAACATTCATCCGGG 3432
                                                                                                                                                                                                                                                                                                                                                    TRECTTGCGCAGCGTG 3348
                                                                                                                                                                                                                                                                                                             FIGUTIGCGCCAGCGTG 5283
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1; DNA; 5285 BP.

rst entry)

ace of a construct comprising the PCV Rep gene.

eplication, RCR; Rep gene, gene function, Geminivirus, virus, gene therapy, PCV; ss.

1WO-US05394.

JUS-0505477.

ALE BIOLOGY CORP.

de capable of rolling circle replication in host, wery of gene function, comprises Rep gene, sequences the polynucleotide and open reading frame encoding est

; 61pp; English.

action describes a polymucleotide that is capable of rolling cation (RCR) in an eukaryotic host. The polymucleotide free encoding from a virus, sequences that are cis on ectide such that he Rep protein can bring about RCR of the de, an open reading frame encoding a protein of interest where the polymucleotide lacks genes of the virus. The ected from the group of genera of family Geminivaridae, and Nanovirus. The polymucleotide sequence is useful for yof the function of genes in eukaryotic hosts, and for enhancing a trait in a host eukaryotic cell, for ing a gene in a plant or in mammalian cell and thus altering inating the function of that gene, as gene sequence delivery manified approaches, for gene therapy applications in whole animal genomics. The present sequence represents of in whole animal genomics. The present sequence represents in whole animal genomics. The present contains the under the transcriptional control of its own promoter, and tive coat protein inactivated by insertion of the bacterial

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4325 GGGCGAACTCCCGCCCCCCCCCGACGCTGCTCTCGGTCATGGCCGCCCGGAGGCGT 4266 3863 TGCTGGTTTCCTGGACGCTGCTGCTGCTGCCGTAGACTCCGCGAGGCTCCA 3922 4265 CCGGGAAGTTCGTGGACGACCTCCGACCACCGCTGCTCACCGCGCGCG	3983 CCAGCATGAGATCCCGGGCTCCAGCGGCGCGCCCCGGAAAACGATTCCGA 4042	4103 TCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCG	4138CTCAGAAGAAATACCGCATCAGGAAATTGTAAGCGTTAATAATACAGAAGAACTC 4150 3845 ATGCGTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATAATTCAGAAGAACTC 3786 4151 GTCAAGAAGGCGATAGAAGGCGATGCGCGCGAATCGGGAGGCGAAACCGTAAAGCAC 4210 3785 GTCAAGAAGGCGATAGAAGGCGATGCGCTGCGCAATCGGGAGCGGCGATACCGTAAAGCAC 3726	4211 GAGGAAGCGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGC 4270	4331 GCCATTTTCCACCATGATATTCGGCAAGCACGCCATGGGTCACGACGAGATCCTC 4390 3605 GCCATTTTCCACCATGATATTCGGCAAGCACGCATGGGTCACGACGAGATCCTC 3546 4391 GCCGTCGGGCATGCGCGCCTTGAGCTGGCAACACATGGGTCACGACGAGGTCCCTGATG 4450	4451 CTCTTCGTCGGGATCATCGACGAGACGGGCTTCCATCCGAGTACGTGCTCGTC 4510	4571 CCGCATTGCCATCAGCCATGATGCTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAG 4630 [4691 GAGCAGAGCTGCGCAAAGAAAGCCCCTCGTCGCCAGCCACGATAGCCGCGTGCTGGTC 4750
4 6 6 6 6	8 8 8 8	8 8 8	8888	8888	8 6 8	8 6 8 6	8 6 6 8	<i></i> ŏ
cloning vector. Sequence 5285 BP; 1216 A; 1277 C; 1514 G; 1278 T; 0 other; Ouery Match Best Local Similarity 80.6%; Pred. Mo. 1.9e-244; Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3; 2942 CTTCCGCTTCCTCGCTCACTGACTCGCTGCGTCGTTCGGCTGCGGCGGAGCGGTT 3001 5285 CTTCCGCTTCCTCCACTGACTCGCTGCGTCGTTCGGCTCGGCGGCGGCGGTT 3001 5285 CTTCCGCTTCCTCAATAGCGGTTATTCCACAGATCAGGGCAGCGGTT 5226 3002 CAGCTCACTCAAAAGCGGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA 3061	2 ACATGTGAGCAAAAGGCCAGGAACGTAAAAAGGCGGGTTGCTGGGGT 5	9 GGGGAAACCGGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGGTCCCTGGTGC		22 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCGACTG	CTAACTACGGCTACACTAGAAGAACGGTTTTGGTATCTGCGCTCTGCTGAAGCCAGTTA	662 GTTTTTTTGTTTGCAAGCAGCAGAATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTT	3782 CATGAGATTATC 3794	03 AAGCGGCCAICGTGCCTCCCCACTCCTGCAGTTCGGGGGCATGGATGCGCGCGATAGCCGC

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3441 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3681 GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC 3740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3081 GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCCATAGGCTCCGCCC 3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2305 GCAGGTGTACTCGAGGCGCGCATCTCGGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3141 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2245 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACAGGACT 2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2005 CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 AAGAACAGTATTTGGTATCTGCGCTCTGCAGTGAAGCCAGTTACCTTCGGAAAAAAGAGTTGG 3620
                                      The invention provides a novel method for directing self-assembly of a gene having three or more fragments in a directionally and spatially ordered fashion to produce a gene vector. The method involves usage of primers, containing class IIS restriction endonuclease recognition sites, for isolation of these fragments. As described in the disclosure, the method may also use a vector for the incorporation and screening of endogenous mouse promoter elements for the incorporation and screening of endogenous mouse promoters. In the example given, plasmid VLSNO2, containing a circularily permuted mouse VL30 genome, was used in the construction of single long terminal repeat (LTR) vectors used in the method of the invention. In general, the method is claimed useful for isolating and identifying regulatory sequences from a cell, including those for enhanced biological activity, or tissue-specific, hormone-specific or developmental-specific gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2125 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1885 GAGGTATGTAGGCGGGTGCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3261 GCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOSS CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels 269; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.6%; Score 1618.2; DB 19; Length 6561; Best Local Similarity 86.7%; Pred. No. 6.1e-242; Matches 1911; Conservative 0; Mismatches 23; Indels 269; G
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6561 BP; 1629 A; 1593 C; 1696 G; 1643 T; 0 other;
Example 3; Pages 110-113; 141pp; English.
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3245 GAGCACAGCTGCGCAAGGACGCCCGTCGTGGCCAGCCACGATAGCCGCCGCTGCCTCGTC 3186
                                           1185 TIGCAGTICALICAGGGCACCGGACAGGTCGGTCTTGACAAAAAAAAGAACGGGCGCCCCTG 3126
                                                                                                                                    1811 CGCTGACAGCCGGAACACGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCCAGTCATA 4870
                                                                                                                                                                   CCCTGACAGCCGGAACACGGCGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATA 3066
                                                                                                                                                                                                                              GCCGAATAGCCTCTCCACCCAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTTCAAT 4930
                                                                                                                                                                                                                                                                         3065 GCCGÁATÁGCCTCTCCACCCAAGCGGCCGGAGACCTGCGTGCAATCCATCTTGTTCAAT 3006
                                                                                                                                                                                                                                                                                                                       CATGCGAAACGATCCTCTCTCTCTTCATCAGATCTTGATCCCCTGCGCCATCAGAT 4990
                                                                                                                                                                                                                                                                                                                                                                  CATGCGAAACGATCCTCATCCTGTCTCTTGATCAGAGCTTGATCCCCTGCGCCATCAGAT 2946
                                                                                                                                                                                                                                                                                                                                                                                                                CCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGG 5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2945 CCTTGGCGGCGAGAAAGCCATCCAGTTTACTTTGCAGGCTTCCCAACCTTACCAGAGGG 2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        885 GGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCG 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5111 CCATGRAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTCCA 5170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2825 CCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTCCCTTGTGCA 2766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5171 GATAGCCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACTGGCTTTCTA 5230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5051 CGCCCCCAGCTGCCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for assembling gene or gene vector - comprises use of primers containing class IIS restriction endonuclease recognition sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class IIS restriction endonuclease recognition site; LTR; andogenous mouse promiter predictio gene expression; hormone-specific gene expression; mouse VL30 genome; developmental-specific gene expression; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid VLSNO2 DNA sequence used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV33630 standard; DNA; 6561 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NATU-) NATURE TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hodgson CP, Xu G, Zink MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0070910.
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δ	3861 GCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAACTCCGCGAGGTCGTC 3920	OY 4941 GATCCTGATCCTGTCTTGATCAGATCTTGATCCCTGCGCCAT
qq	1695	
δλ	3921 CAGCCTCAGGCAGCAGCTGAACCAACTCGCGAGGGATCGAGCCCGGGGGTGGGCGAAGAA 3980	un.
qq	ATTCCGGGGTGGGCGAAGAA 167	654
ζŏ	81 CICCAGCATGAGAICCCCGCGCTGGAGGAICAICCAGCCGGCGGCGGGAAAACGAITCC 404	Oy 5061 GGCATTCGCTTGCTTGCTCATAAAACCGCCCAGTCTAG DD 594 GGCAATTCCGGTTGCTTGCTGTCCATAAAAACCGCCAGTCTAG
qq	CTCCAGCATGAGATCCCCGCGCTGGAGGA	5121
& g	4041 GAAGCCCAACCTTTCATAGAAGGCGGGGGGGGGGAATCGAATCTCGGGATGGCAGGTTGGG 4100	534
Š	1 CGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGGTCAGAAGAACTCGTCAAGAAGG 416	QY 5181 TAGCTGACATTCATCGGGGTCAGGACCGTTTCTGGGACTGGCT Dh 474 TAGCTGACATTCATCGGGACTCAGGACCGTTTCTGGGGAACTGACTCAGTCAG
qa	TTGGTCGTCATTTCGAACCCCA	5241
상 염	4161. CGATAGAAGGCGATGCGCTGCGAATCGGGAGCGCGATACCGTAAAGCACGAAGAGGAGGG 4220 	414 TICCTTTAGCAGCCCTTGCGCCCTGAGTGCTTGCGGCAGCGTG
0,7 0,0	4221 TCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAAGGCTATGTCCTGA 4280	RESULT 8 AB078294 ID ABQ78294 standard; DNA; 2192 BP.
λō	4281 TAGCGGTCCGCCACCCCAGCCGGCCACAGTGAATCCAGAAAAGGGGCCATTTTCC 4340	ABQ78294;
qq	1374 TAGGGGTCCGCCACACCCAGCCGGCCACCAGGATCCAGAAAGCGGCCATTTCC 1315	DT 05-NOV-2002 (first entry)
8 8	41 ACCATGATATTCGGCAAGGAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGC	
QQ Q	ACCATGATATTCGGCAAGCAGGATCGCCATGGGTCACGAGGAGATCCTCGCCGTCGGGC	
දු දු	4401 ATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCC 4460	
Š	61 AGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTC	OS Synthetic. XX XX PN WO200261037-A2.
o o	4 AGAICAICCIGAICGACAAAGACGGGCTICCAICCGAGIACGIGCICGCICGAIGCGAIG	XX PD 08-AUG-2002.
B 04	4521 TTGGCTTGGTGGTGGTGGGGAGTAGCGGATCAAGCGTATGCAGCGGCGGCTGCATTGCA 4580 1134 TTGGCTTGGTGGTCGAATGGGCAGTAGCGGATTGCAGCGGTATGCAGCGGCGCGCGC	
δλ	TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCC	PR 12-DBC-2000; 2000US-25502IP. XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
QC QC	TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCC	(ADVI-) ADVISYS.
දු පු	4641 GGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAGCACGAGCACAGGT 4700	PI Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, XX DR WPI, 2002-619237/66.
<i>₹</i> 5 40	4701 GGGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTGC	XX PT Proproving or enhancing growth, lean body mass, milk pr PT efficiency or Insulin-like Growth Factor-I levels, com PT introducing a vector encoding a growth hormone releasi
ð 1	51 TTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGBACCGGGCGCCCTGCGCTGACAGC	
q d	TTCAGGGCACCGGACAGGTCGGTCTTGACAAAAGAACCGGGCGCCCCTGCGCTTGACAGC	
£ 6	4821 CGGARCACGGGGGGATAGGGRAGGATTGTGTGGCGGTGATAGGGGAGGGATAGGG 4880 6334 CGGARACACGGGGGATTCACAGGCGGATTGTTGTGCCCCAGTCATAGCCGAATAGC 775	
<u>ڄ</u> ۾	4881 CTCTCCACCCAAGCGGCCGGAQAACCTGCGGGCCAATCCATCTTGTTCAATCAATCAATCAA	CC improving or entaining characteristics e.g. growth, re CC Insulin-like Growth Factor (IGF)-1 levels, growth rate CC production in an offspring, and for delaying birth of CC the method comprises introducing a vector, encoding GP
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TTGTCCAGATAGCCCAG 5180
                    ATCAGATCCTTGGCGGC 5000
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rate; milk production; er; ution; ss.

R, Smith RG;

c production, feed comprises asing hormone into

nich was used to normone releasing the used in the sa a method for lean body mass, lean and milk of an offspring.

of the female animal prior to or during gestation of the offspring under conditions where the nucleotide sequence is expressed. The method is useful of improving or enhancing animal growth, for increasing growth hormone, lean body mass, IGF-I levels, feed efficiency, growth rate, ratio of sometotrophs to other hormone-producing cells in a pituteary gland, and milk production in an offspring, and for delaying birth of an offspring. GHRH nucleic medicine, both human and veterinary, e.g. in treating growth-related discorders such as hypoplutitary dwarfism resulting from abnormalities in growth hormone production, and in stimulating the growth and enhancing feed conversion efficiency of animals raised for meat, milk

2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCGGCTCACAATTCC 2765 2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGGTTTCCAGTCGGGAAACCTGTCGTGCCA 2885 2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCGCTTTC 2945 2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGGCGGTATCAGC 3005 3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 3125 3126 CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185 3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245 3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTTCGGGAAGCGT 3305 3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365 3366 GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACGGCTGCGCCTTATCCGGTAACTA 3425 3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAA 3485 3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA 3545 550 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 609 670 Gecechircicaracercacecreraegraphychearicearchaegreericecrecaa 729 790 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCCACTGGTAA 849 70 CTIGGCGTAATCATGGTCATAGCTGTTTTCCTGTGAAATTGTTATCCGCTCACAATTCC 129 190 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGGCCA 249 430 GTGAGCAAAAGGCCAGCAAAAGGCCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT 489 490 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG 549 610 recrerreceaecerececrizacesaracererecescrirerecerrecesarases 669 730 dereserrererecedeneendeecedentendeecedaecedrececerrarecegranera 789 310 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC 369 Query Match 30.4%; Score 1603.8; DB 24; Length 2192; Best Local Similarity 82.8%; Pred. No. 1.2e-239; Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps Sequence 2192 BP; 486 A; 634 C; 601 G; 471 T; 0 other; and egg production. Query Match Best Local Similarity 쉱 g ઠે à 8X888888888888X8 g g ઠ g СP g ò 엄 $\dot{\delta}$ 임 à ò ò 8 ò g ઠે ઠે

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් ඊ සි	3546 CTACGCCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
<u>À</u>	3606 CGGAAAAAGAGTIGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTGGTGGTTT 3665
ે જે	66 TITTGTTTGCAAGGAGCAGTAGTTAGGGGCAGAAAAAAAAGATCTGAAGAAGATCTCTTGAT 372
q	TGA
È	3726, CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT 3785
qq	CTACGGGGTCT
Š	3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATG 3845
Dβ	1108 1108
ò	3846 GATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAA 3905
qq	1108 1107
ò	3906 CTCCGCGAGGTCGTCCAGCCTCAGGCAGCTGAACCCAACTCGCGAGGGATCGAGCCC 3965
qq	1108 1107
δ	3966 GGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGGGGCTGGAGGATCATCCAGCCGGCGTC 4025
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ઠે	4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG 4085
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ò	CTCGTCAAGAAGGCGATAGAAGGCGATGCGCTACGAAATCGGGAGCGGCGATACCGTA
Ф	GATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATAC
Š	4206 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
qq	
ර්	66 AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGGCGCACAGTCGATGAATCCAGAA 432
තු	SGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCC
È	4326 AAGCGGCATTTTCAACATGATATTCGGCAAGCAGGATCGCCATGGGTCACGACGAGA 4385
QQ	acoscantinticaccandanathcoscaascancoccanoscancaca
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q	CTCGATGCGATGTTTCGCTTGGTGGTGGAATGGGCAGGTAGCCGGATCAAGCGTATGC 153
ò	4566 AGCCGCGCATTGCATCACCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC 4625

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4686 ACGICGAGCACAGCIGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4745
                                                                                                                                             5046 GAGGGCCCCCAGCTGGCAATTCCGGTTGCTGTTCCATAAAACCGCCCAGTCTAGC 5105
1538 AGCCGCCGCATTGCATCAGCCATGATGCATACTTTCTCGCAGGAGCAAGGTGAGATGAC 1597
                                        4626 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGACA 468S
                                                                            1598 AGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 1657
                                                                                                                                                                                                     TOGICCIGCAGITCATICAGGGCACCGGACAGGICGTCTTGACAAAAAAAACGGGCGC 4805
                                                                                                                                                                                                                                                                                    CCCTGCCTGACAGCCGGAACACGCGCATCAGAGCAGCCGATTGTGTCTGTGCCCAG 4865
                                                                                                                                                                                                                                                                                                                          1778 CCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCGGATTGTCTGTTGTGCCCAG 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1958 CAGATCCTTGGCGGCAAGGAAGCCATCCAGTTTACTTTGCAGGGCTTCCAACCTTACCA 2017
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                                                                                                                                                                                                                                           1718 TCGTCCTGCAGTTCATTCAGGCCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGC 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass; Insulin-like Growth Rector-1, IGF-1, milk production; feed efficiency; somatotroph; growth-related disorder; hypopituitary dwarfism; meat production; egg production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Improving or enhancing growth, lean body mass, milk production, feed efficiency or Insulin-like Growth Factor-I levels, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kern DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT 5146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2078 AACTGTTGGGAAGGGGGATCGGTGCGGGCCTCTTCGCTATT 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of vector pSPc5-12-HV-GHRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schwartz RJ, Carpenter RH, Draghia-Akli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ78293 standard; DNA; 3534 BP.
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The present sequence represents vector pSPG5-12-HV-GHRH, which carries CDNA encoding pig growth hormone releasing hormone (GHRH) cDNA. Nucleic acids encoding GHRH are used in the method of the invention. The specification describes a method for improving or enhancing characteristics e.g. growth, lean body mass, Insulin-like Growth Facts and milk production in an offspring, or and for delaying birth of an offspring. The method comprises introducing a vector, encoding GHRH, into cells of the female animal prior to or during gestation of the offspring under conditions where the mucleotide sequence is expressed. The method is useful of improving or enhancing animal growth, for increasing growth hormone, lean body mass, IGF-I levels, feed efficiency, growth rate, ratio of somatorrophs or enhancing animal growth, for increasing growth hormone, lean body mass, IGF-I levels, feed efficiency, growth rate, ratio of somatorrophs or other hormone-producing cells in a pituitery gland, and milk production in an offspring, and for delaying birth of an offspring growth-related disorders such as hypopituicary dwarfism resulting from abnormalities in growth hormone production, and in stimulating the growth and enhancing feed conversion efficiency of animals raised for meat, milk and egg production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1532 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2886 GCTGCATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGTATTGGGCGTCTTC 2945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        introducing a vector encoding a growth hormone releasing hormone into an animal before or during gestation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.4%; Score 1603.8; DB 24; Length 3534; Best Local Similarity 82.8%; Pred. No. 1.1e-239; Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 I; 0 other;
                                                                                      Example 2; Page 109-111; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method has been developed of treating urinary incontinence (UI) in mammals. The method comprises delivering a nucleic acid vector for the expression of a growth factor or neurotrophic factor in a tissue or tissues. The present sequence represents the actual lower sequence of plasmid piGOSS2 nucleotides 1-3599 from the present invention. Due to the growth and stimulatory effects of growth factors and neurotrophic factors, introducing these factors to degenerated muscles in the neural inprove UI by enhancing both their integrity and neural innervation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGCGGGTTTGCGGTATTGGGCGCTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                              Score 1603.8; DB 19; Length 3599;
Pred. No. 1.1e-239;
0; Mismatches 27; Indels 392; Gaps
                                                                                                                   ant of urinary incontinence - by delivering nucleic acid for expression of growth factor or neurotrophic factor in
                                                                                                                                                                                                                                                                                                                                                                  Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 other;
                                                                                                                                                                                Disclosure; Page 105-107; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              30.4%;
Dest Local Similarity 82.8%;
Matches 2022; Conservative
                              (GENE-) GENEMEDICINE INC.
                                                                                                                     freatment of urinary
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Best Local Similarity
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04-FEB-1997;
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4386 TCCTCGCCGTCGGCGATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCC 4445
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336 GCTGGGCTGTGTGCACGACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 3425
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                                                                                         716 GCTGGGCTGTGTGCACGCAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA 775
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                                                                                                                                                                                                                                                                     TOGICITGAGICCAACCCGGIAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGIAA
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4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCT 4505
                                                                              4506 CGCTCGATGCGATGTTCGCTTGGTGGTCGAATGGGCCAGGTAGCCGGATCAAGCGTATGC 4565
                                                                                                                     1464 GGCTCGATGCGATGTTTCGCTTGGTCGATGGGCAGGTAGCCGGATCAAGCGTATGC 1523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGF-1; insulin-like growth factor 1; skeletal alpha-actin gene promoter; muscle atrophy; diabetes; osteoporosis; growth disorder; therapy; AIDS; Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss.
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02-DEC-1996;
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This sequence is the actual sequence for pIGO552 which is an example of a vector of the invention. The vector is for expression of a nucleic acid sequence in a cell, and compities: (a) a nucleic acid casecter containing a sequence encoding insulin-like growth factor-1 (IGF-I); (b) a sequence encoding region including a promoter from a sweletal alpha-actin gene; (c) a linker connecting the promoter from a nucleic acid assette, and lacking the coding sequence of a gene with which it is neturally associated; and (d) a 3' flanking region or both, where the arturally associated; and (d) a 3' flanking region or both, where the casestte and comprises a sequence from a growth hormons 3'-UTR. The rector can provide for efficient IGF-I expression, particularly in gene therapy. It can be used for the elivery of IGF-I for treating diseases such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth disperse, genetic disease such as chacch-mark-tooth disease, AIDS, atherogenesis, atherosclerotic, cardlovascular, cerebrovascular, or peripheral vescular disease, haemophilia, inflammation and side-effects from anti-cancer and anti-viral drugs. The vectors can also be used to research or Ilvestock improvement.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duery Match 30.4%; Score 1603.8; DB 19; Length 3599; Best Local Similarity 82.8%; Pred. No. 1.1e-239; Arches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps
                                                                                                                                                                                         New vector for expression of insulin-like growth factor-I -containing a skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3' region from growth hormone 3'-UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3599 BP; 733 A; 1098 C; 1042 G; 726 T; 0 other;
                                                                                                                                                                                                                                                                                                 Claim 16; Page 37-41; 115pp; English.
                                                                                               Coleman M, Demayo FJ, Schwartz R;
                      (BAYU ) BAYLOR COLLEGE MEDICINE. (GENE-) GENEMEDICINE INC.
                                                                                                                                               WPI; 1998-333339/29.
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                                            3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245
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                                                                              537 AAACCCGACAGGACTATAAAGATACCAGGGGTTTCCCCCTGGAAGCTCCCTGGGGCGCTC 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A method has been developed of treating urinary incontinence (UI) in mammals. The method comprises delivering a nucleic acid vector for the expression of a growth factor or neurotrophic factor in a tissue or tissues. The present sequence represents the expected upper sequence of plasmid pigloss nucleotides 1.5800 from the present invention. Due to the growth and stimulacory effects of growth factors and neurotrophic factors, introducing these factors to degenerated muscles in the urinary system can improve UI by enhancing both their integrity and neural innervation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC
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Human; IGF-1; insulin-like growth factor 1; urinary incontinence; gene therapy; neurotrophic factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of urinary incontinence - by delivering nucleic acid vector for expression of growth factor or neurotrophic factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 103-105, 117pp, English.
                                                                                                                                                                                                                                                                                                                                                                         97US-0036862
                                                                                                                                                                                                                                                                                                               98WO-US02051
                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENE-) GENEMEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-437184/37.
                                                                                                                              Homo sapiens.
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                                    1225 AACGCTATOTCCTGATAGCGGTCCGCCACCCAGCCGGCCACAGTGGATGAATCCAGAA 1284
                                                                                           4326 AAGCGCCCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGA 4385
                                                                                                                                    1285 AAGCGGCCATTTTCCACCATCATATTCGGCAAGCAGCATCGCCATGGGTCACGACGAGA 1344
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2946 GGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGGCGGAGCGGTATCAGC 3005

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This sequence is the expected sequence for pIGO552 which is an example of a vector of the invention. The vector is for expression of a nucleic acid agequence in a cell, and compises: (a) a nucleic acid casette containing a sequence encoding insulin-like growth factor-I (IGF-I); (b) a sequence encoding insulin-like growth factor-I (IGF-I); (b) a sequence encoding insulin-like growth factor-I (IGF-I); (b) a sequence encoding region including one or more sequences necessary for skeletal alpha-actin gene; (c) a linker connecting the 5° flanking region of the nucleic assette, and lacking the coding agouence of a gene with which it is naturally associated; and (d) a 3° flanking region, including a coid casette, and lacking the coding sequence of a gene with which it is naturally associated; and (d) a 3° flanking region, including a 3° flanking region or a 3° non coding region of the nucleic acid cassette and comprises a sequence from a growth hormone 3° UTR. The coefficient (Gr I expression, particularly in gene therapy. It can be used for the delivery of IGF-I for treating diseases such as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth as muscle atrophy, diabetes, neuropathy, osteoporosis, and growth a resulting from diabetes, genetic disease such as Type I or Type 2706 CTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765 2826 ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885 176 177 ACTCACATTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 236 237 derecarraareaareaeceaaceeeeeaaaaaeeeeerrieeerarreeeeerriic 296 atherogenesis, atherosclerotic, cardiovascular, cerebrovascular, or peripheral vascular disease, haemophilia, inflammation and side-effects from anti-cancer and anti-viral drugs. The vectors can also be used to create transgenic animals for research or livestock improvement. Chacot-marie-tooth disease; atherogenesis; haemophilia; neuropathy; ss 57 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2886 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTC Query Match 30.3%; Score 1602.2; DB 19; Length 3600; Best Local Similarity 82.8%; Pred. No. 1.9e-239; Matches 2021; Conservative 0; Mismatches 28; Indels 392; Gaps New vector for expression of insulin-like growth factor-I - containing a skeletal alpha-actin gene promoter, IGF-I coding sequences and a 3' region from growth hormone 3'-UTR Sequence 3600 BP; 733 A; 1099 C; 1042 G; 726 T; 0 other; Claim 16; Page 37-41; 115pp; English. Coleman M, Demayo FJ, Schwartz R; (BAYU) BAYLOR COLLEGE MEDICINE. 96US-0031539. 97WO-US21852 97US-0974572 (GENE-) GENEMEDICINE INC WPI; 1998-333339/29. 19-NOV-1997; WO9824922-A1 01-DEC-1997; 02-DEC-1996; 11-JUN-1998. Synthetic. ठ 셤 셤 ઠ d ò g

dū	2.9.7. CGCTTCCTCCATCCACTCCACTCCACTCCACTCCACTCC	q 0	1095 1095
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경	357 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGGATAACGCAGGAAAGAACAAT 3085	qq	11
λο qα	3066 GTGAGCAAAAGGCCAGGAACGCCAGGAACGCCGAAAAGGCCGCGTTGCTGGCGTTTTT 3125 	∂ 8	4146 AACTCGTCAAGAAGGCGATAGAAGGCGGTGCGCTGCGGATCGCGAACGGCGGTGATACCGTAA 4205
8	CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGGGCC 31	<u>\$</u> &	4206 AGCACGAGGAGGCGGTCAGCCCCATTCGCCGCAAGCTCTTCAGCAATATCACGGTAGCC 4265 [
3 8 8	CALAGOCICGOCCCCCCCTGANGGAGCATCCCCCCTGGAAGGGGGCCCCCTGGGAGGGGCCCCTGGAAGGGGCTCCCTCGTGCGCCCCTGGAAGGCTCCCTCGTGCGCCTCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCGCTCCCTCGTGCTCCCTCGTGCTCCCTCGTGCTCCCTCGTGCTCCCTCGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	\$ a	4266 AAGGCTATGTCCTGATAGCGGTCCGCCACACCCGGCCACAGTCGATGAATCCAGAA 4325
G & A		% वृ	4326 AAGGGGCCAITTICCACCAIGAIAITCGGCAAGCAGGCAICGCCAIGGGICACGACGAA 4385
<i>₹</i> 8	GGGGTTTCTTAGGTCCAGGTGTAGGTATCTCAGTTCGGTGAGGTCGTCGGTCCAA 33	ठ व	4386 TCTCGCCGTCGGGCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCAGACCCC 4445
λο qq	GOTGGGCTGTGTGCACCCCCGTTCAGCCGACCCCTGGCCTTATCGGTAACTA 34	ý d	4446 TGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCCTTCCATCCGAGTACGTGCT 4505
S G	TCGTCTTGAGTCCAACCCGGTAAGACGCGACTGTTTTCGCCACTGGCACGCCACTGGTAA 34	ζ, dg	4506 CGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGGGTATGC 4565
8 8	35.00	à 8	4566 AGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAAGGTGAGATGATGAC 4625
) } & 8	CTACGGCTACACTACACACACTACTACTACTACTACTACTCTCTGCTGACTACTACTTACT	ठ व	4626 AGGAGATCTTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
8 8 8	CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACA	8 8	4686 ACGTCGAGCACAGCAGCAGCAGAGAAGAACGCCCGTCGTGGCCACGATAGCCGCGCTGCC 4745
3 & 2	TITIETTTGCAAGGAGCAGCAGATTACGGGGGAAAAAAAAGGATCTCAAGAAAAAAAA	\$ 60 60	4746 TCGTCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAAAA
3 8 8	CTTTTCTACGGGGTCTGACGCTCAGGAAAGAAAACGAAAGCTTAAGGGATTTTGGTCAT 37	ठे <u>व</u>	4806 CCCTGCGCTGACAGCCGGAACACGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAG 4865
3 &	3786 GAGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCATG 3845	<i>à</i> 8	4866 TCATAGCCGAATAGCCTCTCCAACCGCCGGAGAACCTGCGGTGCAATCCATCTTGT 4925 [
음 충	1095 1094	ð :	926 TCAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCAT 4
qq	1095 1094	a &	1885 TCARTCATGCGAAACGATCCTCATCCTCTTGATCAGATCTTGATCCTGCGCCAT 1944
8	CTCCGCGAGGTCGTCCAGCCTCAGGCAGCTGAACCAACTCGCGAGGGGATCGAGCCC 39	경 음	
8 8	1095	<i>8</i> 1	046 GAGGGCCCCAGCTGCCATTCCGCTTGCTTGCTGTAAAACCGCCCAGTTTGC
qq	1095	<u> </u>	2005 GAGGGGCCCCAGGIGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGGTCTAGC 2004 5106 TATCGCCATGTAAGCCCAGTACAAGCTACCTTTGTCTT 5146
δ .	4026 CCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCG 4085	A G	s ActetragaaAggacaatcagtagagacatttagtatt 210

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This invention describes novel expression vector systems containing RNA stability elements from 3. flanking sequences used for establishing expression of a nucleic acid sequence within a tissue. The vectors also facilitate enhanced expression in tissues and target expression with tissue specificity. The expression wectors can be used to treat diseases through gene therapy by targeting the vector to specific tissues. Diseases that can be treated include muscle arrophy associated with neurological, muscular or systemic disease, aging by causing tissues to express trophic factors, haemophilia by causing tissues to express and secrete clotting factor into the circulation, atherogenesis and secrete clotting factor into the circulation, atherogenesis and secrete clotting factor into the circulation, atherogenesis and atherosclerotic cardivoscular, cerebrovascular or peripheral-vascular disease by causing tissues to express factors involved in tissue metabolism. They can be used to replace genes of inherited genetic cells to produce particular proteins or RNA in vitro. To create transpender and particular proteins or RNA in vitro. To create transpender and expensive metabolism the which can be used for research into human diseases, assessing novel therapeutic methods, assessing the effect of chemical and physical carcingens and for studying the effect of chemical and physical carcingens and for studying the effect of chemical and physical carcingens and for studying the effect of chemical and means and proteins controlled expression of the genes they carry and produce a significantly high level of expression. Using 3 UTR sequences reduces the decay rates of the effect of the vectors which decay rates of the decay rates 
                                                                                                                                                                                                                                              Plasmid pIG0335; expression vector; treatment; disease;
RNA stability element; gene therapy; muscle atrophy; neurological;
muscular disease; systemic disease; aging; trophic factor; haemophilia;
clotting factor; atherogenesis; atherosclerotic; cardiovascular;
cerebrovascular; peripheral.vescular disease; hormone deficiency;
diabetes; transgenic animal; carcinogen; regulatory element;
livestock improvement; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5707 BP; 1221 A; 1634 C; 1576 G; 1276 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New expression vector system useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DeMayo FJ, O'Malley BW, Schwartz RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 17-17F; 67pp; English.
                                             AAX88055 standard; DNA; 5707 BP.
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94US-0209846.
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                                                                                                                                               08-SEP-1999 (first entry)
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                                                                                                                                                                                                Plasmid pIG0335 DNA.
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09-MAR-1994;
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                                                                                                                                                                                                                                                       3574 ACACARACARACGAGCCGGAAGCARAAAGTGTAAAAGCCTGGGGTGCCTAATGAGTGAGTA 3633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTTT 3125
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Query Match 30.3%; Score 1602.2; DB 20; Length 5707; Best Local Similarity 82.8%; Pred. No. 1.9e-239; Matches 2021; Conservative 0; Mismatches 28; Indels 392; Gaps

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GGCCTAATGAGTGAGCTA 2825
                                                                            TAAAACCGCCCAGTCTAGC 5105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 392; Gaps 1;
TCTTGATCCCTGCGCCAT 4985
                                      GGGCTTCCCAACCTTACCA 5045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ing a cytomegalovirus interferon alpha e. 3'-untranslated mid pINO961 which the plasmids can be se, particularly cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence, used for particularly cancer
                                                                                                                                                                                                                                                                         negalovirus; CMV;
8; mammal; disease;
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3906 CTCCGCGAGGTCGTCCAGCCTCAGGCAGCTGAACCAACTCGCGAGGGGATCGAGCCC 3965 1098	4086 TGATGGCAGGTTGGCGTCGTTGGTCGAACCCCCAGAGTCCCGCTCAGAAG 4145 1098	4266 AACGCTATGTCCTGATAGCGGTCCGCCACCCCGGCCGCCACAGTCCGATGAATCCAGAA 4325 1228 AACGCTATGTCCTGATAGCGGTCCGCCACCCCCCCCCCC		AGCCGCCGCATTGCATCAGCCATGATACTTTCTCGGCAGGAGCAAGGTGAGATGACATTCTCGGCAGGAGGAGGCAAGGTGAGATGACATTCTCGGCAGGAGGCAAGGTGAGATGATGACTTTCTCGGCAGGAGGCAGGAGGAGGAGATGACTTCTCGGCCAGGAGGAGGATGATGACTTCTCGGCCAGAGCAGGAGGATGATGAGAGCAGACCATCCCGCTTCCGCCTTCAGTGACAAAAGAGAGAG	4686 ACGTCCGACGACGACGACGACGACGACGACGACCACGAGATACCGCCCGC	4806 CCCTGCGCTGACAGCGGAACACGGCGGTTCAGAGCGGCTTGTTGTGCCCAG 4865 1768 CCCTGCGCTGACAGCGGAACACGGCGCATCAGAGCAGCCGATTGTTGTGTGTG
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120 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG	CACTICCICGCTCACTGACTCGCTCGGTCGGTCGGCTGGGGCGAGCGGTGTCGGCGAGCGGTATCAGC 35 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACT 30 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACT 31 GTGAGCAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCGGGTTGCTGCTGCTGTT 31 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGTTGCTGCGGTTTT 31 GTGAGCAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAAGGCCGGTTGCTGCGGTTTTT 47 CCATAGGCTCCGCCCCCTGACGAGAACCGTAAAAAAGGCCGGGTTGCTGGCGGTTTTTT 47 CCATAGGCTCCGCCCCCTGACGACACACAAAAATGGACGCTCAAGTCAGAGGTGCCG 31	3186 AAACCGACAGACTATAAAGATACCAGGGGTTTCCCCTGGAAGGTCAGAGGGGG 539 3186 AAACCGACAGACTATAAGATACCAGGGGTTTCCCCTGGAAGGTCCTCGTGGGGTC 3245 540 AAACCGACAGAGCTATAAGATACCAGGGGTTTCCCCTGGAAGGTCCTCGTGGGGTC 599 3246 TCCTGTTCCACCCTACAGGGTTACCGGATTTCCCCTTGGAAGGGT 3305 600 TCCTGTTCCACACTACCGGATACCTGTCCGCCTTTCTCTTTGGGAAGGT 659 3306 GGGGTTTCTCATAGGTCACGGATACCTGTCGGCTTTCCCTTCGGAAAGGT 659 1306 GGGGCTTTCTCATAGGTCACGGTTACGGATCTCAGTTCGGTGTCGCTTCGCTTCGCTCCATAGAAGGT 659	660 GGCGCTTTCTCATAGGTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCCAA 719 3366 GCTGGGCTGTGCACACAACCCCGTTCAGCCCGACCGCTGCTCCGGTAACTA 3425 720 GCTGGGCTGTGTGCAACCCCCGTTCAGCCCGACCGCTGCCCTTATCCGGTAACTA 779 3426 TCGTCTTGAGTCCAACCCGGTAAGAACGCTTATCGGCTGCAGCAACGAACTA 3485 780 TCGTCTTGAGTCCAACCGGTAAGAACACGACTTATCGCAACGAGCCAACTGGTAA 339	GCCTAA GCCTAA FTACCTT 		CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCAT 378

5046 GAGGGGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 5105 2008 GAGGGCGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGC 2067 4986 CAGATCCTTGGCGGCAAGAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCA 5045
1948 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGCTTCCCAACCTTACCA 2007 δ 업

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Search completed: February 15, 2004, 11:11:36 Job time : 1314 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  OM nucleic - nucleic search, using sw model
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February 15, 2004, 01:53:42 ; Search time 272 Seconds (without alignments) 8572.894 Million cell updates/sec US-09-921-143-36 5283 1 aagcttgaccttatgcgact......tgagtgcttgcggcagcgtg 5283

Title: Perfect score: Sequence: Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

569978 seqs, 220691566 residues

Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1139956

Post-processing: Minimum Match 0% Maximum Match 100%. Listing first 45 summaries

Issued_Patents NA:*
1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		6, Appl	, Appli	9, Appl	o, Appl	, Appli	, Appli	, Appli		6, Appl	, Appli	, Appli	, Appli	, Appli	, Appli	, Appli	2, Appl		3, Appl	, Appli			8, Appl		, Appli	7, Appl	
	Description	Sequence 1	Sequence 1	N	m	Seguence 8	Seguence 7	Sequence 7	Seguence 7	Sequence 2	Sequence 4	Sequence 7	Sequence 6	Sequence 6	Sequence 5	Sequence 5	Sequence 2	Seguence 3	Sequence 2	Sequence 2	Sequence 1	Sequence 2	Sequence 1	Sequence 1	Sequence 1	Sequence 1	
SUMMARIES	ID	US-09-186-002-16	US-09-554-929-1	US-09-380-190A-29	US-09-380-190A-30	US-08-472-809B-8	US-08-948-378A-7	US-09-169-425C-7	US-09-759-960-7	US-09-380-190A-26	US-09-533-220A-4	US-08-751-767A-7	US-08-723-306-6	PCT-US96-10041-6	US-08-723-306-5	PCT-US96-10041-5	US-09-380-190A-22	US-09-554-572-3	US-09-380-190A-23	US-09-554-572-2	US-09-554-572-1	US-09-380-190A-20	US-09-380-190A-18	US-09-380-190A-19	US-09-380-190A-1	US-09-380-190A-17	F
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AGATTATCGTCGACCAAAGCGGCCATCGTGCCTCCCCACTCCTGCAGTTCGGGGGCCATGG
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                                                    ATGCGCGGATAGCCGCTGCTGGTTTCCTGGATGCCGACGGATTTGCACTGCCGGTAGAAC
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                                                         RESULT 2
US-09-554-929-1/C
is Sequence 1, Application US/09554929
patent No. 6521427
general information
if APPLICANT: Evans, Glen A.
TITLE OF INVENTION: A Method for the Complete Chemical
TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes
FILE REFERENCE: P-EA 4749
CURRENT FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 193
SOFTWARE: FastSEQ for Windows Version 4.0
ISEQ ID NO
SEQ ID NO
ILENGTH: 4800
TYPE: DNA
ORGANISM: Artificial Sequence
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33.9%; Score 1793.4;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                         FRATURE:
// OTHER INFORMATION: Synthetic plasmid US-09-554-929-1
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                                                                            CAATCATGCGAAACGATCCTCATCCTGTCTCTTGATCAGATCTTGATCCCCTGCGCCATC
                                                                                                                                        <u> AGGGGGCCCCAGCTGGCAATTCCGGTTCGCTTGCTGTCCATAAAACCGCCCAGTCTAGCT</u>
                                                                                                                                                                                                                                          ATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTGCGTTTTTCCCTTG
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                           CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTT
                                                                                                                   AGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAG
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                                                         CAATCATGCGAAACGATCCTCATCCTGTCTTGATCAGATCTTGATCCCCTGCGCCATC
CATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTT
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US-02-380-190A-29/C
US-02-380-190A-29/C
5 Sequence 29, Application US/09380190A
5 Patent No. 6410220
5 GENERAL INFORMATION:
6 APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
7 APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
7 TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 74
CORRESSONDEMESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT,
STREET: 119 NORTH FOURTH STREET, SUITE
CITY: MINNEAPOLIS
STATE: MINNEAPOLIS
COUNTRY: USA
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APPLICATION NUMBER: PCT/US98/03918
PILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MUTHING, ANN M.
REGISTRATION NUMBER: 33-977
REFFENCE/DOCKET NUMBER: 228.00010201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-380-190A-29
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CLASSIFICATION: <Unknown>
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TELEPAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 5594 base pairs
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STRANDEDNESS: single
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Length
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Score 1652.4;
Pred. No. 0;
0; Mismatches
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                                                                        3431 GTCAGCACCGTTTCTGCGGACTGGCTTTCTACGTGTTCCGCTTCCTTTAGCAGCCCTTGC
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                                                                                                                                                                                                                                                                                      APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND ITHEREOF
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                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: MUSTING, RAASCH & GEBHARDI,
STREET: 119 NORTH FOURTH STREET, SUITE
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <UNKNOWN>
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Pred. No. 0;
0; Mismatches
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APPLICATION UNMERS: PCT/US98/03918
PILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA (genemic)

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-380-190A-30
                                                                                                                      5283
                                                                                                                                             3371 GCCCTGAGTGCTTGCGGCAGCGTG 3348
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REGISTRATION NUMBER: 33,977
REFERENCE DOCKET NUMBER: 22
TELECOMMUNICATION: 11FORWATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                    RESULT 4
US-09-380-190A-30/c
; Sequence 30, Application US/09380190A
; Settent No. 6410220
; GENERAL INPORMATION:
                                                                                                                    5260 GCCCTGAGTGCTTGCGGCAGCGTG
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INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 6561 base pairs
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STRANDEDNESS: single
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Best Local Similarity 86.7%;
Matches 1911; Conservative C
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1314 ACCORDING CONTROL CONTR	; Patent No. 25.5564; Sebert J.; GENERAL INFORMATION: APPLICANT: Schwartz, Robert J.; APPLICANT: Schwartz, Fanco J.; APPLICANT: Deflayyo, Franco J.; APPLICANT: O'Malley, Bart W.; IITLE OF INVENTION: Expression Vector Systems and
3261 CCCGCTTACCGGGATACCTGTCGGCTTACCCGTACGGGCTTTCTCTCTATG 2320	

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                                                       3934 ccaradecrococococordadeacardadaaaarocaceocoaagicaeagood
                                                                                                                                                                                               4054 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT
                                                                                             3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCTCCTTC
                                                                                                                                    3994 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC
                                                                                                                                                                       TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT
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; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                COMPUTER: DESCRIBED COMPUTER: DESCRIBED COMPUTER: DESCRIBED CORPUTER: DESCRIBED CONTRACTOR SYSTEM: IBM P.C. DOS 5.0 SCHWARE: WORD PERÍCCE 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/472,809B FILING DATE: MARCH 9, 1995 FILING DATE: MARCH 9, 1994 APPLICATION NUMBER: 08/209,846 FILING DATE: MARCH 9, 1994 APPLICATION NUMBER: 07/789,919 FILING DATE: NO. 5925564ember 6, 1991 AND MARCH 103-04-04
TITLE OF INVENTION: Method of Use NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 8uite 4700 CITY: Los Angeles STREET: California COUNTRY: U.S.A. ZIP: 90071-2066 COMPUTER READABLE FORM: MEDIUM TYPE: Storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.8%;
Matches 2021; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA
US-08-472-809B-8
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATING SYSTEM: Windows95
SOCHWARE: FESISEG for Windows Version 2.0
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/948,378A
FILING DATE: 09-CCT-1997
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGBNT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE POCKET NUMBER: 08191/004001
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELEPAX: 617-542-8906
TELEPAX: 617-542-8906
TELEPAX: 1017-543-8906
                                       IMMUNOGENIC PEPTIDES FROM THE HPV E7 PROTEIN 19
                                                                                                                  NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGEN
TITLE OF INVENTION: THE HPV F
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: sing
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                                                     4622 AGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4681
                                                                                                                                                          AACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGAGTCGAATCCAGAA 4325
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GENERAL INPORMATION:
APPLICANT: Urban, Robert G. APPLICANT: Chicz, Roman M. APPLICANT: Chicz, Roman M. APPLICANT: Collins, Edward J.
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RESULT 6 US-08-948-378A-7/c

2445 3307 2325 GICTIGAGICCAACCGGTAAGACACGACTIAICGCCACIGGCAGCACCACIGGTAACA 3487 3008 ACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 3067 2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTTTCC 2505 3247 2444 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 2385 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 3367 2324 GGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC 2265 3368 IGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC 3427 2264 TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCCTTATCCCGGTAACTATC 2205 3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGGTTGCTGGCGGCTTTTTCC 2504 ATAGGCTCCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGGGGGCGAA 3188 ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGTGG 2384 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGG Query Match 29.7%; Score 1571.6; DB 3; Length 4665; Best Local Similarity 86.3%; Pred. No. 0; Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps TOPOLOGY: circular MOLECULE TYPE: pBIOTOPEHPV

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                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                  Score 1571.6; DB 3;
Pred. No. 0;
0; Mismatches 114;
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NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819
REFERENCE DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPA: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: MOLECULE TYPE: DNA
US-09-169-425C-7
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.3%;
Matches 1850; Conservative
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                            4748 GICCIGCAGIICATICAGGGCACCGGACAGGICGGICTIGACAAAAAAAAACCGGGCGCC 4807
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APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                       524 AATCATGCGAAACGATCCTCATCCTGTCTTTGATCGATCTTTG 481
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastsEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
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APPLICATION NUMBER: 09/169,425
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 617-542-6070
                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09759960 Patent No. 6582704
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ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
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Best Local Similarity 86.3
Matches 1850; Conservative
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IDNESS: double
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US-09-759-960-7
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STRANDEDNESS:
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US-09-759-960-7/c
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Page 12

GENERAL INFOR ; APPLICAN ; TITLE OF	NUMBER O CORRESPO	STR CIT	ZIP COMPUTER NED COM	OPE SOF	FIL CLA PRIOR AP	ATTORNEY	TELECOMM	INFORMATION F SEQUENCE	MOLECULE TOP SEQUENCE SEQUENCE	Query Match Best Local Simi	Macches 1849; Oy 3008 ACT		Db 1955 GAG Qy 3128 ATA	Db 2015 ATA Qy 3188 ACC	Db 2075 ACC		3308 CGC	Db 2195 CGC
3968 GGTGGGGAAGAACTCCAGCATGAGATCCCCGCGGTGGAGGATCATCCAGCCGGCGTCCC 4027 	4028 GGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGGGGGGG	4088 ATGGCAGGTTGGGCGTCGTTGGTCGATCTTCGAACCCCAGAGTCCCGGTCAGAAGAA 1147	4148 CTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAG 4207 	4208 CACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267 	4268 CGCTATGTCCTGATAGGGGTCCGCCACCCCGGCGGCGCCACGCGGATGAATCCAGAAAA 4327 	4328 GCGCCCATTTTCCACCATGATATTCGGCAAGCATCGCCATGGGTCACGACACACAAAC 4387 	4388 CTCCCCGTCGGCCATGCGCCCTTGAGCCTGGCGAACAGTTCGGCTGGCGGAGCCCCTG 4447	4448 AIGCICTICGICCAGATCAICCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCG 4507 	4508 CTCGAIGCGAIGTTTCGCTIGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAG 4567 	4568 CCGCCGGATTGCATCAGCCATGATACTTTCTCGGCAGGAGCAAGGAGAGTGAGATGACAG 4627 	4628 GAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC 4687	4688 GTCGAGCACAGCTGCGCAAAGAACGCCCGTCGTGGCCAGCCA	4748 GTCCTGCAGTTCATTCAGGGCACGGACAGGTCTTGACAAAAAAAA	4808 CTGCGCTGACAGCCGGAACACGGGGATCAGAGCAGATTGACTGTTGTGCCCAGTC 4867 	ATAGCCGAATAGCCTCTCCACCAAGCGGCGGAGAACCTGCGTGCATCTTGTTC		4928 AATCATGGGAAAGGATCTTCATCTGTCTTGATCTG 4971 -	
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RESULT 9 US-09-380-190A-26 Sequence 26, Application US/09380190A ; Fatent No. 6410220

3368 IGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAIC 3427
2255 IGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCCTATCCGGTAACTAIC 2314 CCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC 3247 GITCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAGCGTGG 3307 SCTITCICALAGGICACGCIGIAGGIAICICAGIICGGIGIAGGICGIICGCICCAAGC 3367 CGCTTTCTTATACTCACACGCTGTATCTCAGTTCGGTGTATCTCAGTCGTCGTTCGCTCCAAGC 2254 TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT 3067 GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCC 3127 GCAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCC 2014 AGGCTCCGCCCCCGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAA 3187 29.7%; Score 1570; DB 4; Length 4518; .larity 86.2%; Pred. No. 0; Conservative 0; Mismatches 115; Indels 180; Gaps NT: NATURE TECHNOLOGY CORPORATION, ET AL. INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF ZIP: 55401

UTER READABLE FORM:

UNER READABLE FORM:

COMPUTER: 1E0PDY disk

COMPUTER: 1EN FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

BNT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,190A

FILING DATE: 26-Aug-1999

CLASSIPICATION: «Unknown» ONDENCE ADDRESS:
DRESSER: MUBTING, RAASCH & GEBHARDT, P.A.
EBET: 119 NORTH FOURTH STREET, SUITE 203
TY: MINNEAPOLIS
ATE: MINNESOTA APPLICATION NUMBER: PCT/US98/03918
PILING DATE: 28-FEB-98
RWEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKT UNMBER: 228.00010201
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
NW FOR SEQ ID NO: 26:
SNCE CHARACTERISTICS: POLOGY: linear E TYPE: DNA (genomic) E DESCRIPTION: SEQ ID NO: 26: NGTH: 4518 base pairs 'PE: nucleic acid 'RANDEDNESS: single OF SEQUENCES: UNTRY: USA ilarity à 셤

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GCCGATTGTCTGTTGTCCCAGTC 4867
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                                                                            GGTAGCCGGATCAAGCGTATGCAG 4567
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                                                                                                                                                               CAGCCACGATAGCCGCGCTGCCTC 4747
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                                                                                                                     3548 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAGGCCAGTTACCTTCG 3607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1570; DB 2; Length 6139;
Pred. No. 0;
0; Mismatches 115; Indels 180;
APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENT: PC-DOS/MS-DOS
SOFTWARE: PACENT: READABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENT: READABLE
OPERATING SYSTEM: BOS NOV-1996
CURRENT APPLICATION NUMBER: 36 663
REFERENCE CANDONER: 36 663
REFERENCE CANDONER: 117-221
TELEPHONE: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: DISP DAGE PAIRS
TELEPHONE: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: LINGTH: ACID
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity
Matches 1849; Conser
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US-08-751-767A-7
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REFERENCE/DOCKET NUMBER: 2549
TELECPHONICATION INFORMATION:
TELEPHONE: 801531918
TELEPHONE: 801531918
TELEPHONE: 801531918
TELEPHONE: ROLES IN NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 8797 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECTLE TYPE: other nucleic acid
DESCRIPTION: taurus beta casein 5' regulatory region plus genes encoin the parameter of the casein 5' regulatory region plus genes in TYPE: maphipathic peptide and green fluorescent protein"
HYPOTHETICAL: YES
MATI-SENSE: NO
US-08-723-306-6
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Pred. No. 0;
0; Mismatches 112; Indels
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Best Local Similarity 86.3%;
Matches 1847; Conservative
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US-08-723-306-6/C
US-08-723-306-6/C
Sequence 6, Application US/08723306
Patent No. 5856178
Patent No. 5856178
Patent No. 5856178
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Patent No. 7856178
Patent 
                                                       CTCGCCGTCGGGCATGCGCGTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTG
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION: 800
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NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
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TELECOMMUNICAL
TELEFAX: 8015319168
TELEFAX: 8015319168
TELEFAX: 8015319168
TENGRATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGRAT and 19 and see pairs
TOPOLOGY: not relevant
FOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Construct comprising Bos
DESCRIPTION: /desc = "Construct comprising Bos
DESCRIPTION: taurus beta casein 5' regulatory region plus genes encod
DESCRIPTION: amphipathic peptide and green fluorescent protein"
TAL: TES
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10041
FILING DATE:
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SWEJGET PHD, SUSAN E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801531922
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00 00 00 00 00 00 00 0	Qy 4693 GCACAGCTGCGCAAGGAACGCCGTCGTCGTCGCCACCATAGCCGCCTCCTCCT 4752 Db 6933 GCACAGCTGCGCAAGCACCCGTCGTGGCCACCACCACTCCTCTCT 6874 Qy 4753 GCAGTTCATTCAGGACCCGGACAGCCAGCCACCAGCCTCGCG 4812 Db 6873 GCAGTTCATTCAGGACACGGACAGCTCTTGACAAAAGAACGGGCCCCTGCG 6814 Qy 4813 CTGACAGCGGACACGGACAGGACGCGTTTGACAAAAAAAA
	Db 8073 ACGGGGTCTGACGCAAAGCGAAAGTCGCGTTAAGGGATTTTGGTCATGAGATTA 8014 3793 TCGTCGACCAAAGCGCATCGTGCT

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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11093 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECTLE TYPE: other nucleic acid
DESCRIPTION: 'desce "Construct comprising
DESCRIPTION: portions of Bos raurus beta casein gene and genes encoding
DESCRIPTION: amphipathic peptide and green fluorescent protein"
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRATURE:
NAME/KEY: excn
LOCATION: 1801..1834
OTHER INFORMATION: /product= "beta casein excn 1"
Sequence 5, Application US/08723306
Patent No. 5856178
GENERAL INFORMATION
APPLICANT: White PhD, Kenneth
APPLICANT: White PhD, John
APPLICANT: White PhD, John
APPLICANT: Reed, William
TITLE OF INVENTION: Pegitides in Mammalian Transgenic Organisms
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRES: 32
CONDUTER: D. Box 2250
CITY: Salt Lake City
STATE: Utah
CONDUTER: Day Gits
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURASIFICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION NUMBER: US/08/723,306
FILING DATE:
CLASSIFICATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
TELEPHONE: PATENCE PATENCE
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NAME/KEY: exon
LOCATION: 3780.3832
OTHER INFORMATION: /product= "beta casein exon 1"
PEATURE:
NAME/KEY: TATA signal
LOCATION: 1766.1773
FEATURE:
NAME/KEY: exon
LOCATION: 4567.4590
OTHER INFORMATION: /product= "portion of beta casein of the case of the casein of the case of the casein of
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NAME/KEY: 5'UTR
LOCATION: 127.1800
OTHER INFORMATION: /function= "5' flanking regulatory
OTHER INFORMATION: region of bovine beta casein gene"
OTHER INFORMATION: region of bovine beta casein gene"
NAME/KEY: mat peptide
LOCATION: 4587.5310
OTHER INFORMATION: /product= "Green fluorescent
OTHER INFORMATION: protein"
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10849 CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10789 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10729 TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                    3013 AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11089 ATGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3073 AAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCGCCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCG
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                                                                                                                                                                                                                                                                                                                                                 Indels 180; Gaps
                                                                                                                                                                                                                                                                              Length 11093;
                             FEATURE:

NAME/KEY: polyA_signal

LOCATION: 7630...7635

COTHER INFORMATION: /standard_name= "Bovine beta casein
OTHER INFORMATION: 3' region, in exon 9"
US-08-723-306-5
OTHER INFORMATION: /product= "Shiva-1 coding sequence"
                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                       Score 1569.8; DB 2;
Pred. No. 0;
0; Mismatches 112;
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.3%;
Matches 1847; Conservative
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8990
   9109 CTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGC 9050
                                                           4873 CGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAATCA
                                                                                                             PCT-USS6-10041-5/c
; Sequence 5, Application PC/TUS9610041
; GENERAL INFORMATION;
; APPLICANT: White Phb, Kenneth
; APPLICANT: Morrey Phb, John
; APPLICANT: Reed, William
; TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
; TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
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TELEFAX: 8101512121
TELEFAX: 8101512121
SEQUENCE CHARACTERISTICS: 820UBNCE CHARACTERISTICS: 1.ENGTH: 1.1093 base pairs
TYPE: nucleic acid sTRANDENESS: 40uble
TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid BESCRIPTION: 40es = "Construct comprising DESCRIPTION: portions of Bos taurus beta casein gene and genes DESCRIPTION: amphipathic peptide and green fluorescent protein"
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NAME/KEY: exon
LOCATION: 4567..4590
OTHER INFORMATION: /product= "portion of beta casein OTHER INFORMATION: exon 3"
FEATURE:
                                                                                                                                                                           4933 IGCGAAACGAICCICAICCIGICTIGAICAGAICTIG 4971
                                                                                                                                                                                                              8989 TGCGAAACGATCCTCATCCTGTCTTTG 8951
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LOCATION: 3780..3832
OTHER INFORMATION: /product= "beta casein exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "beta casein
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ZIP: 84110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vexi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10041
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Sweigert PhD, Susan E
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 254;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 8015321922
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NAME/KEY: TATA signal
LOCATION: 1766..1773
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: Y
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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10189 CTGGGCCTTCACCCGAACTTGGGGGGGGGGGGGGAAAAGGAAAAAGGAAAAATGCGGGGTAT 10130
                                                                                                                                               10070
                                                                                                                                                                                                                                                                   10069 CGTTTÅTGAÅCAACGACCCAACACGTGCGTTTTATTCTGTCTTTTATTGCCGTCATA 10010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9830
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OTHER INFORMATION: /function= "5' flanking regulatory
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OTHER INFORMATION: /standard_name= "Bovine beta casein
CTHER INFORMATION: 3' region, in exon 9"
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                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                             Query Match
29.7%; Score 1569.8; DB 5;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 112;
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9470

4512 9410 4572 9350 4632 9290

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                                        4693 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCACCACGATAGCCGCGCTGCCTCGTCCT 4752
                                                               9229 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCTT 9170
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Search completed: February 15, 2004, 05:49:54 Job time : 350 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 15, 2004, 05:29:07; Search time 1682 Seconds (without alignments) 11569.936 Million cell updates/sec nucleic search, using sw model OM nucleic -Run on:

US-09-921-143-36 5283 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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2449703 segs, 1841816367 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 36, Appl	Sequence 16, Appl	⋖	16,	ä	10	11	12	Sequence 13, Appl	Sequence 14, Appl	Sequence 15, Appl	Sequence 9, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 4. Appli
	d di	US-09-921-143-36	US-10-198-478-16	US-10-322-360-1	US-10-286-186-16	US-10-038-001-1	US-10-021-403A-10	US-10-395-709-11	US-10-395-709-12	US-10-395-709-13						
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Appli	Appli	Appli	Appli	Appl	Appl	Appli	Appli	Appl	Appli	Appl	Appli	Appli	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
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29.7	29.7	29.7	φ.	a)	g	29.7	29.7	φ.	29.7	29.7	29.7	29.7	29.7	φ.	29.7	29.7	σ.	σ.	ď,	٥.	6	φ.	6	φ.	S)	φ.	φ.	29.7	٠.
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16	17	18	13	50	21	.55	23	24	25	56	27	58 28	59	30	31		33	34	35	36		38	39	40	41	42	43	44	45
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ALIGNMENTS

ö TACCATGGTGATGCGGTTTTTGGCAGTACATCGGCGTGGATAGCGGTTTGACTCACG 120 TACCATGGTGATGCGGTTTTTGGCAGTACATCGGCGTGGATAGCGGTTTGACTCACG 120 121 GGGATTICCAAGICTCCACCCCACTGACGICAATGGGAGTTTGTTTTGGCACCAAAATCA 180 9 9 1 AAGCTTGACCCTTATGCGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 1 AAGCTIGACCTIAIGCGACTITCCIACTIGGCAGIACAICTACGIAITAGICAICGCIAI 0; Gaps DB 13; Length 5283; Indels 0 Query Match
100.0%; Score 5283;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5283; Conservative 0; Mismatches 61 61 දු පු 8 셤 8

180

181 ACGAGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240

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1311 ACMORNOGRATICONTOGRANCOMACOMACOMACOMACOMACOMACOMACOMACOMACOMA
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181 ACGAGCTRUCTAMANTOTOTIANCAMANTOTOTIANAGAGGGGADAMANGACCOSTS 300 241 MACNITOTIANCTAMACGGGGGTTANACCOCCUTATANAGAGGGGADAMANCACCOSTS 300 241 ACCATICACTRUCTAMACGGGGGTTANACCOCCUTATANAGAGGGGADAMACCACCOSTS 300 242 CATACCCGGATTCOTOGGGGGTTANACCGGTTANACCGGGTTANACCCCCGGTTANACCGGGTTANACCCCCGGTTANACCGGGTTANACCGGTTANACCGGTTANACCGGGTTANACCG

NAME/KEY: misc_feature	Db 5911 CTTGGCGTAATCATGGTGATAGCTGTTTCCTGTGTGAAATTGTTATCGCTCACAATTCC 5976	Db 6091 GCTGCATTAATCGCCAACGCCGGGAAGAGGGGTTTGCGTATTGGGCCCTCTTC 6150 Qy 2946 GGCTTCCTCGCTCACTGACTGGCTGCGGTCGTTCGGCTGCGGGGGGGTTTTGCGTATCAGC 3005 Db 6151 GGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGGAGCGGTATCAGC 6210 Qy 3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065 Db 6211 TCACTCAAAGGCGATAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 6270 Qy 3066 GTAGCAAAAGGCCAAAAGGCCAGAACGGGAAAAAGGCGGTGGCTGCTGGTTTTT 3121	Db 6271 Gradianaldisceadanaldisceadanalanaldisceadanalanalanaldisceadanalanaldisceadanalanaldisceadanalanalanalanalanalanalanalanalanalan	6451 3306 6511 3366 6571	6631 TCGTCTTGAGTCCAACCCGGTAAGACACTTATCGCCACTGGCAGCAGCTGGTAA 3486 CAGGATTAGCAGAGGGAGGTATGTAGGCGTGCTACTTGAAGTGGTGGCCTAA 6691 CAGGATTAGCAGAGGGAAGGTATGTAGGGGTCTTCTGAAGTGGTGGCCTAA 5546 CTACGGCTACACTAGAAGAACAGTATTTGGTACTGCGGTTCTTGAAGTGGTGCCTAA 5546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGGTTCTTGTGAAGCCAGTTACCTT 6751 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGGTCTGCTGAAGCCAGTTACCTT 6751 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGGTCGTGTGTGT
Db 4561 TATGCAGCCGCCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAG 4620	4741 CTGCCTCGTCCTGCAGTTCATTCAGGGCACCGGCACGGTCTTGACAAAAAGAACGGGCACCGGCCTCGCCTCGCACACGCGACACGGCCATTGTCTTGTG 4801 GGCGCCCCTGGCCTGACAGCCGGAACACGGCGCATTCATCTGTG 4801 GGCGCCCCTGGCCTGACAGCCGGAACACGGCGCATTCATCTTGTG 4861 CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCGGAGAACCTGCAATCCAT 4861 CCCAGTCATAGCCGAATAGCCTCCCACCCAAGCGGCGGGGAGAACCTGCGTGCAATCCAT 4861 CCCAGTCATAGCCGAATAGCCTCCCACCCAAGCGGCCGGAAACCTGCGTGCAATCCAT 4861 CCCAGTCATAGCCGAATAGCCTCCCCCCAAGCGCCGGAGAACCTGCGTGCAATCCAT CTTTGTTTCATAGCCGAATAGCCTCCTCCACCCCAAGCGCCGGAGAACCTGCGTGCAATCCAT	4921 CTIGITIONALCATGCGAAAAGGATCCTCATGCTGTCTTGATCAGATCTTGATCCCTGC 4981 GCCATCAGATCCTTGGCGGCAAGAAAGCCATCCTGTCTTTGATCAGGGCTTCCCAACCT 4981 GCCATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCT 4981 GCCATCAGAGCCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCT 5041 TACCAGAGGGCCCCCAGCTGGCAATTCCGTTTGCTTTGC	5101 CTAGCTATCGCCATGTAAGCTCACTGCAAGCTACCTGCTTTCTCTTTGCGCTTTTTTTT	> 0 88 0 E	TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox FILE REFERENCE: 38-21 [13347] B CURRENT APPLICATION NUMBER: UG/10/198,478 CURRENT FILING DATE: 2002-11-12 PRIOR APPLICATION NUMBER: 09/186, 002 PRIOR PILING DATE: 1998-11-04 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin version 3.1 SEQ ID NO 16 LENGTH: 8349 TYPE: DNA ORGANISM: artificial sequence FEATURE: CHER INFORMATION: completely synthesized FEATURE:

	5046 8107 5106 8167 5126 5226 5226	RESULT 3 US-10-322-360-1/c i Sequence 1, Application US/10322360 i Publication No. US20030165946A1 GENERAL INFORMATION: APPLICANT: Evans, Glen A. ITLE OF INVENTION: A Method for the Complete Chemical ITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes ITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes CURRENT APPLICATION NUMBER: US/10/322,360 CURRENT FILING DATE: 2002-12-17 PRIOR APPLICATION NUMBER: US 09/554,929 PRIOR FILING DATE: 2000-05-12 NUMBER OF SEQ ID NOS: 193 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 4800 TYPE: DNA ORGANISM: Artificial Sequence FRATURE: OTHER INFORMATION: Synthetic plasmid	Ouery Match Best Local Similarity 91.8%; Pred. No. 0; Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1; Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1; Qy 3127 CATAGGCTCCGCCCCTGACGACGATCACAAAATCGACGCTCAAGTCAGAGGTGGCGA 3186 Db 4800 CATAGGCTCCGCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA 4741 Qy 3187 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAGGCTCT 3246 Db 4740 AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGTGGCGTCT 4681 Qy 3247 CCTGTTCCGACCGCTGCTACCGGATACCTGCTCCTCGTGGGAAGCTCT 4681
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116	RESULT 4 US-10-286-186-16/c US-10-286-186-16/c ; Sequence 16, Application US/10286186 ; Publication No. US20030143741A1 ; GENERAL INFORMATION: ; APPLICANT: PALMER, KENNETH E. ; APPLICANT: POGUE, GARY P. ; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION ; TITLE OF INVENTION: VECTOR ; FILE REPERENCE: 00801017900US00 ; CURRENT APPLICATION NUMBER: US/10/286,186
CCCGTTCCCGCCCTCCCGCTTACCGGATACCTGCCGCCTTTCTCCCCTCGGGGACCTGG GGCCTTTCTCATAGCTCACGCTTACGGATACCTGGTGATGGTGTTACGCGTTACGCGTAGGTGTTCCCAAG GGCCTTTCTCATAGCTCACGCTGTAGGTACTCCCAGTGGTGGTGGTGGTTGGT	4207 GCACGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

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Pred. No. 0;
0; Mismatches 206; Indels 231; Gaps
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/505,477
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 5225
                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.7%;
Matches 2087; Conservative
                                                                                                                                        TYPE: DNA
; ORGANISM: Porcine Circovirus
US-10-286-186-16
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4145 GGGTCACGTCCCGGACCACCGGCGAAGTCCTCCACGAAGTCCCGGGAACC 4086 3983 CCAGCATCGTCCTCCGGACCACCGGCGAAGTCCCCGGAAGTCCCGGGAACC 4086 4085 CGAGCCGGTCGACCGCTGGAACTCGACGCTCCGGCGCGCGC	4211 GAGARGCGCTCAGCCCATTCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCCCAACGC 4270 4211 4AGGARGCGCTAGCCCATTCGCCGCAAGCTCTTCAGCAATATCACGGGTAGCCCAACGCCGAAGACCCAACGGAAAACCC 4330 4331 4341 43

GGGGTGGGGAAGAACTCCCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTC	Db 1958 CAGATCCTTGGCGGCAAGAAAGAAAGCATTACTTTGCAGGCTTTCCAACCTTACCA 1107	TGATGGCAGGTTGGGCGTCGCTTGGTCGTCATTTCGAACCCCCAGAGTCCCGCTCAGAAG AACTCGTCAAGAAGGCGATCGAGGCGATCGCGATCGCGGAGGCGCGGATCCGTAA AACGCTCAAGAAGGCGATCGAGGCGATCGCGCCCCAAGGTCCTCAGAAGTCCGTCAAAAGAACGCGATCAGAAAGGCGATCCCCCCCC		TICATICAMAGGCGGTAMTACGGTTMTCCACAGAMTCAGGGGATTAACGCAGAAAGAACAT 1065 TICACTCAAAGGCGGTAATACGGTTMTCCACAGAMTCAGGGGATTAACGCAGGAAAGAACAT 129 GTGACCAAAGGCCGCACAAAAGGCCCAGGAAACGCCGCGTTGCTGGCGTTTTT 1125 GTGACCAAAGGCCCACAAAAGCCCCGTAAAAACGCCCGGTTGCTGGCGTTTTT 1489 CCATAGGTTCCCCCCTCTACAAAAACCACACAAAAATCCAACCTCAAGTCAAGTCAGGGGTTGCTGGCGTTTTT 1489 CCATAGGTTCCCCCCTCTACAAAAACCACACACACACACA
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1.5 ACCRETATION CONTINUES 1.5	The properties of the properti	AACTCGTCAAGAAGAGGCATTAGAAAGGCAATGCGATTGCGAATCGGGAGCGGCGAAAAAAAA		GTGAGCAAAAGGCCAGCAAGAACCGTAAAAAGGCCGCGTTTTT 489
Contraction	Contract	AACTCGTCAAGAAGGCCATAAAAGGCCATGCGGTTGCCGAATCGGGAAGCGGGGATACCGTAA 		G GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCTG
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RESULT 7 US-10-395-709-11 Sequence 11, Application US/10395709 Sequence 11, Application US/10395709 Sequence 11, Application US/10395709 GENERAL INFORMATION: APPLICANT: Advisys TITLE OF INVENTION: GLUTAMATE ("PLG") SYSTEM FILE REFERENCE: 108328.00115 - AVGI-0021P1 FILE REFERENCE: 108328.00115 - AVGI-0021P1	CURRENT REPLICATION NUMBER: US/10/395,709 CURRENT FILING DATE: 2003-03-24 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin version 3.1 SEQ ID NO 11 LENGTH: 3534 TYPE: DNA	components	Query March 50.4%; Score Lous.8; DB 12; Dength 3534; Best Local Similarity 82.8%; Pred. No. 0; Matches 2022; Conservative 1; 2706 CTAGACGTAATGAGGTCATAGGTTTCCTGTGTAATTGTTATCGCTCACAATTCC 2765	Db 1412 CTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTAATTGTTATCCGCTCACAATTCC 1471 Oy 2766 ACACAACATACGAGGAAGCATAAAGTGTAAAGCCTGGGGGTGCCTAATGAGTGAG	2826 ACTCACATTAATTGCGTTGCGCTCACTCCGGGGTATCCGGGGAAACCTGTCCGTGCCAGTGGCCTGTGCCTGTGCGTGC	OY 2886 GCTGCATTAATGAATCGCCCAACGCGGGGGGGGTTTGCGTATTGGGCGCTCTTC 2945	Oy 2946 CGCTTCCTCGCTCACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTATCAGC 3005	OY 3006 TCACTCAAAGGGGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3065 Db 1712 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 1771	Oy 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAAAAAGGCCGCGTTGCTGCGGTTTT 3125 Db 1772 GTGAGCAAAAGGCCAGGAAAAGGCCAGGAACGTAAAAAAGGCCGCGTTGCTGGCGTTTTT 1831	1832 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAAGAGGCGCGCGC	3246 TCCTGTTCCGACCCTGCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGGGT	OY 3306 GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA 3365	Oy 3366 GCTGGGCTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGGCCTTATCCGGTAACTA 3425 Db 2072 GCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGACTA 2131

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Qy 5106 TATCGCCATGAAGCCCACTGCTACTGCTTTCTCTT 5146 Db 3420 AACTGTTGGAAGGGCATCGGTGCGGGCCTCTTCGCTATT 3460	RESULT 12 US-10-021-403A-9 i Sequence 9, Application US/10021403A j Publication No. US20030074679A1 i GENERAL INFORMATION: j APPLICANT: Advisys j TITLE OF INVENTION: Growth in Offsepring j TITLE OF INVENTION: Growth in Offsepring j TITLE OF INVENTION: Growth in Offsepring j CURRENT APPLICATION NUMBER: US/10/021476/OTA 00-91 j CURRENT FILING DATE: 2002-04-11 j PRIOR PILING DATE: 2002-04-12 j PRIOR FILING DATE: 2000-12-12	OS: 11 Version 3.1	This is a r on.	Query Match 30.4%; Score 1603.8; DB 15; Length 3534; Best Local Similarity 82.8%; Pred. No. 0; Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;	Oy 2706 CTAGACGTAATCATGGTCATAGCTGTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765	Qy 2766 ACACAACATACGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG	Oy 2826 ACTCACATTAATTGCGTTCACTCACCTCACTTCCAGTCGGGAAACCTGTCGTGCCA 2885	Qy 2886 GCTGCATTAATGAATCGGCGAGAGAAGGCGGTTTGCGTATTGGCTCTTC 2945	Oy 2946 CGCTTCCTCGCTCACTGACTCGCTCGGTCGTTCGCTGCGGCGGGGGTTCGGTACAGC 3005	Qy 3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCACGGGATAACGCAGGAAAGAACAT 3065	Qy 3066 GTGAGCAAAAAGGCCAGGAAAAGGCCAGGAAAAAGGCCGCGTTGCTGGCGTTTTT 3125. Db 1772 GTGAGCAAAAGGCCAGGAAAAGGACCAGGAACCGTAAAAAAGGCCGGGTTGCTGGCGTTTTT 1831	Oy 3126 CCATAGGCTCCGCCCCTGACGACGACCATCACAAAATCGACGCTCAAGTCAGGGGGG 3185 Db 1832 CCATAGGCTCCGCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG 1891	AN 3186 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 3245 1892 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC 1951	QY 3246 TCCTGTTCCGACCCTGCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT 3305
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                                                                                             Gaps
                                                                                          392;
                                                                   Length 5966;
                                                                                          Indels
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                                                                                          0; Mismatches
                                                                Score 1600;
Pred. No. 0;
            FEATURE:

COTHER INFORMATION: Mouse IL-12 pIN0961
US-10-136-837-3
                                                                30.3%;
Similarity 83.5%;
5; Conservative
ORGANISM: Artificial
                                                              Query Match
Best Local Simi
Matches 2005;
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                                                                                        1768 CCCTGCGCTGACAGCCGGAACACGGCGCATCAGAGCAGCGATTGTCTTGTTGTGCCCAG
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US-09-759-960-7/c

i Sequence 7, Application US/09759960
; Patent No. US20010006639A1

GENERAL INFORMATION:
APPLICANT: Collins, Roward J.
APPLICANT: Collins, Edward J.
APPLICANT: Edward J.
APPLICANT: 2010-2804
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
COMPUTER: IBM Compatible
OPPERATIOR TREABABLE FORM:
MADORESSEE: Fish & RICHARS
COMPUTER: IBM Compatible
OPPERATION NUMBER: US/09/759,960
FILING DATE:
PRICATION NUMBER: 09/169,425
FILING DATE:
APPLICATION NUMBER: 03/169,425
FILING DATE:
ATTEMENT FRASET NUMBER: 01191/004002
TELECOMMUTATION INPORMATION:
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TELEX: 200154
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
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Score 1571.6; DB 9; Length 4665;
Pred. No. 0;
0; Mismatches 114; Indels 180; Gaps
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                                        0;
Query Match
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Matches 1850; Conservative
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Oy 4928 AATCATGCGAAACGATCCTGTCTGTGTTGATCAGATCTTG 4971	RESULT.15 US-10-128-853-4/c ; Sequence 4, Application US/10128853 ; Publication No. US20030003536A1 ; GENERAL INFORMATION: ; APPLICANT: Mcintyre, Peter ; APPLICANT: James, lain Fraser	TITLE OF INVENTION: Human Vanilloid Receptor FILE REFERENCE: 4-30875A CURRENT APPLICATION NUMBER: US/10/128,853 CURRENT FILING DATE: 2002-04-23 PRIOR APPLICATION NIMBER: 115/09/533,200	FRIOR FILING DATE: 2000-03-23 ; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1 ; PRIOR FILING DATE: 1999-03-26 ; NUMBER OF SEO ID NOS: 4	; SOFTWARE: PatentIn Ver. 1.30 ; SEQ ID NO 4 ; LENGTH: 4886 . TVPR: NA	sus	Query Match 29.7%; Score 1570; DB 15; Length 4886; Best Local Similarity 86.2%; Pred. No. 0; Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps	3008	3068	Oy 3128 ATAGGCTCCGCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAA 3 Db 4175 ATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGTCAAGTCAAGGTGGCGAA 4175 ATAGGCTCCGCCCCCTGAGGAGATCAAAAATCGACGCTCAAGTCAAGGTGGCGAA 4		3248	3308	Oy 3368 IGGGCTGTGTGCACGAACCCCCCTTCAGCCCGCCGCGCCTTATCCGGTAACTATC 3	Qy 3428 GTCTTGAGTCCAGCGGTAAGACACGACTTATCGCCACTGGCAGCAGCAGCTGGTAACA 3	Oy 3488 GGATTAGCAGCGAGCTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT 3 Db 3815 GGATTAGCAGAGGTATGTAGGGGGGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACT 3	QY 3548 ACGGCTACACTAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG) 2y 3608 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTT 3
3947 TCGCGAGGGGATCGA 3961 	3962	4028 GGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTG 4087 	4088 ATGGCAGGTTGGGCGTCGCTTGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAA 4147 1364 ATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAA 1305	4148 CTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGCAGCGGCGATACCGTAAAG 4207 	4208 CACGAGGAAGCGGTCAGTTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267	4268 CGCTATGTCCTGATAGCGGTCCGCCACCACCGGCCACACGTCGATGAATCCAGAAAA 4327 	4328 GCGGCCATTTCCACCATGATATTCGGCAAGGCATCGCCATGGGTCACGACGAGTC 4387	4388 CICGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCTG 4447	4448 AIGCICTICGICCAGAICAICCIGAICGACAAGACCGGCTICCCAICCGAGIACGIGG 4507	CTCGATGCGATGTTTCGCTTGGTGGATGGCCAGGTAGCCGGATCAAGCGTATGCAG	4568 CCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAG 4627 	4628 GAGATCCTGCCCGGGCACTTCGCCCAATAGCAGCCAGCCA	4688 GTCGAGGACAGCAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTC 4747	GTCCTGCAGTTCATTCAGGGCACGGACAGGTCGTCTTGACAAAAAAAA	CTGCGCTGACACCGGAACACGGGGATCAGAGCAGCCGATTGTCTGTGCCCAGTC	ATAGCCGAATAGCCTCTCCACCCAAGCGGCCGGAGAACCTGCGTGCAATCCATCTTGTTC	584 AIAGCCGAAIAGCCCCCCAAGCGGCCGGAGAACCGGCGTGCAATCCATCTTGTTC 525

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BG680319 MODEL 0572
BZ57291 MODEL 047
BZ57291 MODEL 047
BZ57391 MODEL 077

OM nucleic

Run on:

Sequence:

Title:

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramarsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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DG680919
CA488579
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BE579291
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HTC: CAP trapper.
Mus musculus (house mouse)
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SOURCE
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AUTHORS
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AU081137 AU081137
AU081124 AU081124
CB686151 BN01b_020
                                                                                                                    ; Search time 9963 Seconds (without alignments)
12887.739 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                     22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                  nucleic search, using sw model
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B2573391 msh2 3083 B2573391 msh2 3083 B2571572 msh2 1950 B1180988 UNL-P-F2-AL633845 AL633845 AL643164 AL643164 AZ67930 ENTLO84TF BQ660293 HG1N05w BC55852 HF01022w BC55822 HF01022w BC57832 msh2 5785 BQ660197 HG1G17w BQ660197 HG1G17w

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GGEVKAREGKOLEBOLASVSSYDBLMSYLYPDYWKMYKCOLAKGGWOOPTLNTFTGDS
VKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGAAINTFFKPPCVSVYRCGG
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CQCVCKRTCPRNQPLNPGKCACGCTENTQKCFLKGKKFFHQTCSCYRRPCANRLKHCD
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                                                                                                                                                                                                                                                                                                                                                                                                              translation="MHLLCFLSLACSLLAAALIPSPREAPATVAAFESGLGFSEAEPD"
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/note="unnamed protein product; putative
vascular endothelial growth factor C (MGD|MGI:109124,
GB|NW 009506, evidence: BLASTN, 99%, match=1784)"
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Pred. No. 6.1e-266;
0; Mismatches 180; Indels
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|clone="C130004M09"
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Matches 1121; Conservative
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Arakawa,Y., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Osazaki,Y., Gojobori,T., Beno,H., Kasukawa,T., Saito,R.,
Radota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischman,M., Gasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Fesole,G., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Fletcher,C., Fultu,M., Garibold,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Wynshaw Beris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y. Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
Punttional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Faruno, M., Haranco, K., Hirzoka, T., Hirzano, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itoh, M., Kono, H., Kouda, M., Koya, S., Kurihara, C., Marsuyama, T., Miyazaki, A., Murata, M., Nashi, K., Nomura, K., Miyazaki, A., Murata, M., Nashi, K., Nomura, K., Sakai, 
                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sawi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384 format Genome Res. 10 (11), 1757-1771 (2000)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length Phase I conas Nature 420, 563-573 (2002)

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FEATURES Location/Qualifiers 1.1667 /organism="Concorbynchus mykiss" /mol_type="mRNA" /db_txef="taxon:8022" /clone="KI2" /tissue_type="kidney" /tissue_type="kidney" /clone="Ione-Tipse"/clone="Concorbynchus mykiss Kidney infected by . infectious hematopoietic necrosis virus" /note="common name:rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name:rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name:rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus" /note="common name: rainbow trout ; infected by infectious hematopoietic necrosis virus"	Query Match 17.9%; Score 948; DB 9; Length 1067; Best Local Similarity 98.8%; Pred. No. 4.2e-254; Anatches 976; 2; Matches 976; Conservative 0; Mismatches 10; Indels 2; 2; Qy 2706 CTAGACGTAATCATGGTCATAGCTGTGTGAAATTGTTATCCGCTCACAATTCC 2765 Db 82 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCGCTCACAAATTCC 141	Qy 2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG	Qy 2886 GCTGCATTAATGAATCGGCCAACGGGGGGGAGAGGCGGTTTGCGTATTGGGGTCTTC 2945 Db 262 GCTGCATTAATGAATCGGCCAACGCGGAGGAGGGGGTTTGCGTATTGGGCTCTTC 321 Qy 2946 GGCTTCCTCGCTCACTGACTGGCTCGGTCGTTCGGCTACGGGGGGGG	3006 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3 382 TCACTCAAAGGCGGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT 3 382 TCACTCAAAGGCGGTAATACGGTTATCCACAGAATTCAGGGGATAACGCAGGAAAGAACAT 4	3066 442 3126	Db 502 CCATAGGCTCCGCCCCCTGACGAGATCGACGCTCAAGTCAGGGCG 561 Oy 3186 AAACCCGACAGGACTATAAAGATACCAGGATTCCCCTGGAAGCTCCTGTGCGCTC 3245 562 AAACCCGACAGGACTATAAAGATACCAGGCTTTCCCCTTGTGCGCTC 621 Oy 3246 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGCCCTTTCTCCCTTCGGGAAGCT 3305 Db 622 TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT 681 Oy 3306 GGCGCTTTCTCATAGCTCAGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT 681 Oy 3306 GGCGCTTTCTCATAGCTCAGGTTCTCAGTTCGGCTTACCCGTAACTCCAA 3365 Db 682 GGCGCTTTCTCATAGCTCAGGTTACTGGTTCAGTTCGGTTACCGGTAACTA 741 Oy 3366 GCTGGGCTGTGTGCACGTAGGTACTCAGTTCGGTTAGGTCGTTCGCTCCAA 3485 Db 742 GCTGGGCTTGTGTGCACGAACCCCCGTTCAGCCGTTATCCGGTAACTA 801 Oy 3426 TCGTCTTGAGTCCAACCCCCGTTCAGCCCGTCGCGCCTTATCCGGTAACTA 801 Oy 3426 TCGTCTTGAGTCCAACCCCCGTTCAGCCCATGGCAGCACCCTCGTAA 3485 Db 742 GCTGGGCTTGTGTGCAACCCCCGTTCAGCCCATGGCAGCACCCTCGTAA 3485 Db 742 GCTGGGCTTGTGTGCAACCCCCGTTCAGCCCATGGCAGCACCCCTTATCCGGTAACTA 801 Oy 3426 CCGGGTTGTGTGCAACCCCCGTTCAGCCCATGGCAGCACCTGGTAA 3485 Db 742 GCTGGGCTTGTGTGCAACCCCCGTTCAGCCCATGGCAGCACCCTCGTAA 3485 Db 862 CAGGATTAGCAAACCCCGGTTAAGACCCCATGGCAGCACCACTGGTAA 3485 Db 862 CAGGATTAGCAAACCCCGGTTAAGACCCCATGGCAGCACCACTGGTAA 3485 Db 862 CAGGATTAGCAAACCCCGGTTAAGACCCCATTATCGCCACTGGTAA 3485 Db 862 CAGGATTAGCAAACCCCGGTTAACACACACTTATCGCCACTGGTAACTTAA 921 Db 862 CAGGATTAGCAAACCCCGGTTAACACACACTTATCGCCACTGGTAACTTAATCTTGAAATTCTTGAAATTCTTGAAATTCTTGAAATTCTTGAAATTCTTGAAATTCTTGAAATTGTTAAAATTCTTTAAAATTCTTTAAAATTCTTTAAAATTCTTTAAAAATTCTTTAAAAATTAA 921 DD 862 CAGGATTAGCAAACCCCGGTTAAGACCCCCTTATCTTTATCTTTAATTCTTTAATAAAATTAAAATTAAAATTAAAATTAAAAAA
	1321 ACGIGCCGAIGCCIGGCICAGCAGGAITTTAITCTTTTATTCAAATGTTGAAGATGACTCA 978 1321 ACGGATTCCATGACATCTGTGGACCAAAGAGGAGCTGGATGAAGGACCTGTCA 138 979 ACCAATGGATTCCATGATGTCTGTGGACCCAACAAGAGGAGCTGGATGAAGACCTGTCAG 103 1381 TGTGTCTGCAGAGGGGGGTTCGGCCTGCCAGCTGGACCCCACAAAGAAGACTAGAAGA 144	1441 A 1441 A 1099 G 1501 G 1159 G	CTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAA	Db 1279 GGGAAGAÁGTTCCACCATCAACATGCAGTTGTTACAGAAGACCGTGTGCGAATCGACTG 1338 Qy 1681 AAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTGT	41 IGGAAAAGACCACAAATGAGCTAATCTAGGATCCGTACCCTGCCCAGGCTTTT 1793 	MUOSILY 2 AUOSILY 2 AUOSILY 2 LOCUS DEFINITION AUOSILY Concordynchus mykiss Kidney infected by infectious hematopoietic necrosis virus Oncordynchus mykiss CDNA clone KI2, mRNA sequence. ACCESSION AUOSILY 1 G1:6431485 SOURCE ONCORDYNCHUS mykiss (rainbow trout) ORGANISM COCCHYNCHUS mykiss (rainbow trout) AUOSILYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostem; COCCHYNCHUS MOCORDYNCHUS mykiss DOCOCHYNCHUS mykiss COCCHYNCHUS MOCORDYNCHUS MACHAZOA; Chordata; Craniata; Vertebrata; Euteleostem; Actinopterygii; Neopterygii; Teleostei; Euteleostei; CORGANISM COCCHYNCHUS MACHAZOA; Analysis of Kidney and Gill Tissues from Hematopoietic Necrosis Virus AUTHORS KONO,T., Sakai,M. and LaPatra,S.E. TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Hematopoietic Necrosis Virus JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001) CONDECT: Masahiro Sakai Faculty of Agriculture Myazaki University 1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan Email: m.sakai@cc.miyazaki.uac.jp.

QY 2946 CGCTTCCTCGCTCACTGACTCGCTGGGGCGGCGGCGGGGGGGG	Oy 3186 AAACCGGACAGGACTATAAAGATACCAGGGCTTTCCCCCTGGAAGCTCCTCGTGCGCTC 3245	Oy 3366 GCTGGGCTGTGTGCACCCCCTTCACCCCGACCGCTGCGCCTTATCCGGTAACTA 3425 Db 743 GCTGGGCTGTGTGCACCACCCCGTTCACCCGACCGCTGCGCCTTATCCGGTAACTA 3425 Qy 3426 TCGTCTTGAGTCCAACCCGGTAAGACACGACCGCTGCGCCTGCTGGTAA 3485 Db 803 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGTAA 862 Qy 3486 CAGATTAGGAGAGAGACACGGTAAGACTATCGCCACTGGTAA 862 Qy 3486 CAGATTAGGAGAGAGAGACACGGTAAGACTTCTTGAAGTTCTTCTTAACAAGTTTCTTGAAGTTCTTTCAAGTTCTTTCT	Cy 3545 actacgctacactagaagaacagtatttcgtatctgcgctctgctgaagccacttacct 3604 Db 923 actacggctacactagaagaacagtatttcgtatctgcgctctgctggagccacttacct 982 Cy 3605 TCGGAAAAGAGTTGTATTTGTATCTGCGCTCTGCTGGTGGTACCT 982 Cy 3605 TCGGAAAAGAGTTGGTAGCTCTT-GATCCGGCAAACAACCACCGCTGGTAGCGGT 3660 Db 983 TCGGAAAAAGAGTGGTAGCTCTTGGATCCGGCAAACAACCGCTGGGAAGGGGG 1042 Cy 3661 GGTTTTTTGTTTGCAAGCA-GCAGATTACGGCAAAAAAAAAGGAT 3706 Db 1043 TGTCTTTTTGTTTGCAAGCA-GCAGAATTACGCGCAAAAAAAAAGGAT 1089	RESULT 4 CB686151/c LOCUS DEFINITION BH01b 02008 A BH01b APC ECORC transgenic Brassica napus overexpressing BNCBF17 c ONSTITUTION BH01b 02008 A ACCESSION CB686151 CB
Oy 3546 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605 Db 922 CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605 Start	AU081124 AU081124 Oncorhynchus mykiss Kidney infected by hematopoietic necrosis virus Oncorhynchus mykiss mRNA sequence. AU081124 AU081124.1 G1:6431472 EST. Oncorhynchus mykiss (rainbow trout) Oncorhynchus mykiss (rainbow trout) Actinopererygii, Neoperaygii, Telesos Portebris Portebris Mathoria mykiss (rainbow trout) Actinopererygii, Neoperaygii, Telesos Portebris Portebris Actinoperaygii, Neoperaygii, Telesos Portebris Portebris Actinoperaygii, Selmaniata, Selmaniata	REFERENCE 1 (bases 1 to 1089) AUTHORS KOND.T., Sakai,M. and LaPatra,S.E. TITLE Expressed Sequence Trag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorpynchus mykiss) Infected with Infectious Hematopoietic Necrosis Virus JOURNAL Mar. Bitcechnol. 2 (5), 493-498 (2001) COMMENT Contact: Masahiro Sakai Faculty of Agriculture Myazaki University Myazaki University 1 - 1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan Email: m.sakai@cc.miyazaki-u.ac.jp.	FEATURES Location/Qualifiers 1. 1089 / Organism="Oncorhynchus mykiss" / Mol_type="mRNA" / Ab_zref="laxon:8022" / Clone="KG'12" / Clone="KG'12" / Clone="KG'12" / Clone="KG'12" / Clone="Lib="Concorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus" / Note="Common name:rainbow trout; infected by infectious hematopoietic necrosis virus" / Note="Common name:rainbow trout; infected by infectious hematopoietic necrosis virus" / Note="Common name:rainbow trout; infected by infectious corigins" / Note="Common name:rainbow	Query Match 17.4%; Score 919.8; DB 9; Length 1089; Best Local Similarity 97.2%; Pred. No. 3.5e-246; Matches 979; Conservative 0; Mismatches 22; Indels 6; Gaps 4; Oy 2706 CTAGACGTAATCATGGTCATAGCTGTTAATTGTTAATCGCTCACAATTCC 2765 Db 33 CTTGGCGTAATCATGGTCATAAGTGTTAAAGTGTAAATTGTTAATCGCTCACAATTCC 142 OY 2766 ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCTCAATGAGTGAG

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University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 206216954
Fax: 2066857244
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/organism="Pseudomonas:
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                   Contact: Singh,J.A.

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Location/Qualifiers
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Unpublished
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966 bp DNA linear GSS 17-DEC-2002
mmb2_1513.x1 mmh Pseudomonas aeruginosa genomic clone mmh2_1513,
genomic survey sequence.
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299 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 240
                                                                                                                    TCCAAGCTGGGCTGTGCACGAACCCCCGTTCAGCCCCASCGCTGTATCCGGT 180
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Pseudomonas aeruginosa
Bacteria; Perudomonas aeruginosa
Bacteria; Peeudomonadaceae; Pseudomonadaceae; Pseudomonadaceae; Pseudomonadaceae; Pseudomonadaceae; Pseudomonas.

(bases 1 to 966)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                      AACTATGCTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGSAGCAGCCACT
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/clone="mmA2 1513"
/clone lib="mmh"
/note="Environmental isolate. Whole genomic shotgun
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                                                                                                             /organism="Oncorhynchus mykiss"
/mol type="mkNA"
/db_xref="taxon:8022"
/clone="xB1"
/clone="xB1"
/clone lib="oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 GCTGCATTAATGAATCGGCCAACGCGGGGGAGGAGGGGGGTTTGCGTATTGGGCGCTTTTC
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Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                  Length 1163;
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Pred. No. 3.1e-207;
0; Mismatches 3;
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Best Local Similarity 99.5%;
Matches 794; Conservative
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       TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA 273
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Oncorpynchus mykiss (language formation)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1163)
Kono, T., Sakai, M. and LaPatra, S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (S), 493-498 (2001)
Contact: Masahiro Sakai
Faculty of Agriculture
                                                                                               GCAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTTTTCCAT
                                                                                                                                       AGGCTCCGCCCCCCTGAGGAGCATCACAAAATCGAGGCTCAAAGTCAGAGGTGGCGAAAC
                                                                                                                                                                               AGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC
                                                                                                                                                                                                                             CCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCT
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                                                    GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT
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3425

3482

759

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 831)

NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CONTACT: Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAMIOG13 row: o column: 04
High quality sequence stop: 810.
                                                                                                                                                                                                                                                                                                                   TAACAGGATTAGCAGAGGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC 3542
                                                                                                                                                 CAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA 3422
                                                                                                                                                                                                                                                                                                                                                                                                  3543 TAACTACGGCTACACTAGAAGAAGAACAGTATTTGGTATCTGCGGCTCTGCTGAAGCCAGTTAC 3602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3663 ITTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT 3722
                                                                                                                                                                                                                                                              640 CTATCGTCTTGAGTCCAACCCCGTAAGACACGACTTATCGCCACTGGCAGCAGCAGCCACTGG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG680919 831 bp mRNA linear EST 01-MAY-2001
602628716F1 NCI_CGAP_SKn4 Homo sapiens cDNA clone IMAGE:4753755 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                        760 TAACTACGCCTACACTAGAACAGTATTTTGTATCTGCGCTCTGAAG-CAGNTAC 818
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  CTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCCTTCGGGAAG
                                                                                                                                                                                         580 CAAGCTGGGCTGTGTGCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA
                                                                                                                                                                                                                                   CTATCGTCTTGAGTCCAACCCGGTAAGACACACGACTTATCGCCACTGGCAGCAGCCACTGG
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/lab host="DHIOB (TI phage-resistant)"
/clone lib="NOI CGAP Skr4"
/note="Organ: skin, Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                               520 CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTC
                                                                  CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCACGTTCGGTGTAGGTCGTTCGCTC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4753755"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 AGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGGATAACGCAGGAAAGAA 279
                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacea; Pseudomonas.

(Dases 1 to 1249)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCGCTTCCTCGCTCACTGACTGCGTTGCGTCGTTCGGCTGCGGCTGCGGCGAGCGGTATC
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/db_xref="maxon:287"
/done="lb="mab"
/note="Environmental isolate. Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 781.2; DB 29; Length 1249; Pred. No. 3.2e-207;
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/mol type="genomic DNA"
/strain="MSH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 20668757244
Email: Graymond@u.washington.edu
Class: shotgun.
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  3486 CAGGATTAGCAGAGCGAG 3503
                          1146 CAGGATTAGCAGAGCGAG 1163
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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LOCUS

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ACCESSION

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/note="Vector: pCMV-SPORT6; Site_l: EcoRV; Site_2: Not I;
Subtracted with Drain, liver, lung, kidney and muscle.
Subtracted with Drain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HWB1
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                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 858)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: Gappbe-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LiNL at:
Plate: LiaM14279 row: 1 column: 15
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                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                  Homo sapiens (human)
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light (250 Bm-2sec-1) and 16 oC / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."

223 c 238 g 182 t 1 others
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                                                                                                                                                                                                                         2701 GCTGTCTAGACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACA 2760
                                                                                                                                                                                                                                                                                                                            2761 ATTCCACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG 2820
                                                                                                                                                                                                                                                                                                                                                                                                                         2821 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 2880
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                                                                                                                                                                                                                                                                                                                                                             633
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                                                                                                                                                                                                                                                                          812 GCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 INTITCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGGTCAGAGG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 TAAACTATCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCAG-CAC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              692 AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 CGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA
                                                                                                                                                                             2; Gaps
                                                                                                                      Query Match
14.8%; Score 780.6; DB 14; Length 833;
Best Local Similarity 99.0%; Pred. No. 3.6e-207;
Matches 805; Conservative 1; Mismatches 5; Indels 2;
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/clone="Manolb_04j14"
/tissue_type="fcutth" leaf"
/dev_stage="3 weeks seedling grown at room temperature"
/clone_lib="Banolb_AAPC_ECORC_transgenic_Erassica_napus_ove
rexpressing_BNOSER7_constitutively_frost_tolerant"
/note="weetch: Bluescript Sk+Xkhol-EcoR1; Site 1: EcoR1;
Site_2: Xhol; Germinated in soil flats and seedlings grown
for 3 weeks in a conviron E-15 cabinet set at 200c /ls hr
                                                                                                                                                                                                                 Bnolb_04j14 A
Bnolb_04fC_ECORC transgenic Brassica napus overexpressing BNCBF17 c
onstitutively_frost_tolerant Brassica napus cDNA clone BnOlb_04j14,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica napus (rape)
Brassica napus (rape)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
i eurosids II; Brassicales; Brassicaceae; Brassica.
(Dases 1 to 833)
Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A., Expressed Sequence Tags from constitutively frost tolerant
transgenic_Brassica napus overexpressing BNCBF17
                   1303 GAIGCIGGAGAIGACICAACAGAIGGAITCCAIGACAICTGIGGACCAAACAAGGAGCIG 1362
                                                                                                                   1363 GATGAAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACCC 1422
                                                                                                                                                                                                                                                                                                                    TGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCA 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1603 CAGAANIGCTIGTIAAAAGGAAAGAAGTICCACCACCAAACAIGCAGCIGIIACAG-ACG 1661
                                              421 GATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCTG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA linear EST 09-APR-2003
                                                                                                                                                    661 TGCCCCAGAAATCAACCCCTANATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 CAGAAATGCTTGTTAAAAGGAAGGATCCACCACCAAACATGCAGCTGTTACAGAACG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby, Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1662 GCCATGTACG-AACCGCCAGAAGGC--TTGTGAGCCAGGATTTT 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 GCCATGTACGAAACCGCCAGAAAGCCTTTGTGAGCCANGAATTT 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Westar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  833 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: singhja@em.agr.ca.
Location/Qualifiers
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(613) 759-1701
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TITLE

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3367 CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT
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Location/Qualifiers
1. .1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic
/strain="MSH"
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Contact: Chris K. Raymond
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356 c
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Best Local Similarity 95.6
Matches 797; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
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                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                     Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Włemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2) Emils wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Genome Project.

No r1 sequence available.
This clone (DKF2p434C17) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de.
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 954)
Ansorge, W., Benes, V., Krieger, S., Mewes, H.W., Gassenhuber, J.
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Pred. No. 2.8e-205;
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ilarity 100.0%; Fred. No. 2.8
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msh2_6285.x1 msh Pseudomonas aeruginosa genomic clone msh2_6285,
genomic survey sequence.
BZ579291
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Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates
Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
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/clone="msh2_6285"
/clone=line="msh"
/note="Environmental isolate. Whole genomic
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Pred. No. 1.5e-199;
0; Mismatches 35;
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tex: 2066857244
Email: craymond@u.washington.edu
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Burns, J. L., Kaul, R. and Olsen, M. V.

Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
Gontact: Christ K. Raymond
Genome Center
University of Washington

Box 352145, Seattle, WA 98105-2145, USA
Faz: 2066857244

Email: craymond@u.washington.edu
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pacs2-164_8370.x1 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_8370, genomic survey sequence.
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Spencer, D.H., Raymond, C.K., Smith, B.E., Sims, B.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
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Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                        3375 IGTGCACGAAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xref="taxon:287"
/clone="pacs2-164_8370"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
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University of Washington
Box 352145, Seattle, WA 98105-2145, USA
12 2062857244
Eax: 2066857244
Email: craymond@u.washington.edu
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Contact: Chris K. Raymond
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msh2_2771.x1 msh Pseudomonas aeruginosa genomic clone msh2_2771, pseudomonas aeruginosa genomic clone msh2_2771, pseudomonas seruginosa genomic clone msh2_27711, pseudomonas seruginosa genomic clone msh2_27711,
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S Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Bredomonas aeruginosa library
J. J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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Pred. No. 3e-196;
0; Mismatches 110; Indels 8;
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/close_lib="mgh"
/note="Environmental isolate. Whole genomic
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    1346
    /organism="Pseudomonas/mol_type="genomic DNA"
    strain="MSH"

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clone="msh2_2771"
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Pseudomonas aeruginosa
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Best Local Similarity 87.9%;
Matches 855; Conservative
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Search completed: February 15, 2004, 19:07:05 Job time : 9974 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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is the number of results predicted by chance to have a

Pred. No.

BD136066 Novel pro BD136064 Novel pro BD136064 Novel pro BD136064 Novel pro BS59416 Signal pept AX360741 Sequence AX360741 Sequence AX5691955 Sequence BD000145 Vector ha 105430 Sequence 16 108105 Sequence 3 M64941 Human cytom M64940 Human cytom M64940 Human cytom M64941 Human cytom BD00013 Vector had 105393 Sequence 14 108103 Sequence 14 108103 Sequence 1 A10617 Human Cytom AR028792 Sequence AR028794 Sequence AR050544 Sequence AR041121 Sequence AR241123 Sequence AR241121 Sequence BD145112 Methods a BD145112 Methods a E00836 Recombinant 149834 Sequence 2 149834 Sequence 2 VRL 28-APR-1993 K03104 Human cytom AX282811 Sequence Rous sarc K02374 Rous-assoc A85308 Sequence 6 BD107647 FIV vacci A92081 Sequence 5 A92080 Sequence 4 AR230690 Sequence A92077 Sequence 1 AR230692 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Rous-associated virus type 2
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.

1 (bases 1 to 1560)
Bizub, D., Katz, R.A. and Skalka, A.M.
Mucleotide sequence of noncoding regions in Rous-associated virus-2: comparisons delineate conserved regions important in replication and oncogenesis AR230688 linear ALEENV 1560 bp ss-RNA Rous-associated virus-2 env and gag genes. ALIGNMENTS SUMMARIES 108105 HSSPIE1AB HSSPIE1AE HSSPIE1AF HSSPIE1AC AF052428 ALELTR2 BD136066 BD136065 BD136064 AX256412 AX591955 BD000145 A10617 AR028792 AR028794 AR050544 A85308 BD107647 AR241123 BD131785 BD145110 BD145112 I49836 HS5IEE AX282811 AR094363 AR241121 AR230692 ALEENV E59416 149834 ВВ GI:210069 Length Query Match Score DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE RESULT 1 ALEENV LOCUS Result No.

.416,5097. .6920)

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Direct Submission
Submitted (04-MAR-1998) Fox Chase Cancer Center, 7701 Burholme Ave,
Philadelphia, PA 19111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PBAWVDSÝQGSFTKPKALPPAÍFLI CGDRAWGGI PSR ÞVGGPCYLGKLTMLAPNHTDI
LKI LANSSRTGI RRKRSVSHLDDTCSDEVQLWGPTAR I FASI LAPGVAAAQALKEI ER
LACWSVKQANLTTSLLGDLLDDVTS I RHAVLQNRAAI DFLLLAHGHGCEDVAGMCCFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDEPSELQLIGSQSLPNITNITRIPSVAGGCIGFTPYDSPAGVYGWDRREVTHILLTD
PGNNPFFDKASNSSKPFTVVTADRHNLFMGSEYCGAYGYRFWEMYNCSQMRQNWSICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVWGRGPPENWCTSTGGTWVNQSKEFNETEPFSFTVNCTGSNLGNVSGCCGEPITILP
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PWPVSEQPAVSLAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDSGADITIISE
EDMPTDWPVVDTANPQIHGIGGGIPWRKSRDMIELGVINRDGSLERPLILFPAVAMVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSDHSESIQKKFQLMKEHVNKIGVDSDPIGSWLRGLFGGIGEWAVHLLKGLLLGLVVI
LLLVVCLPCLLQIVCGNIRKMINNSISYHTEYKKLQKAYGQPESRIV"
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Lyspgswdpitaalsoramvigksgelktwglvlgalkaareegvtsegakfwlclgg
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ADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAAPST
LTTPGEIIKYVLDRQKIAPLTDQGIAAAMSSAIQPLVMAVVNRERDGQTGSGGRARRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MEAVIKAVLTGYPGETSKKDSKKKPPATSKKDPEKTPLLPTRV
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AEVEALMSSPLLPHDVTNIMRVILGPAPYALMMDAWGVQLQTVIAAATRDPRHPANGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCNCATASAPPPYVGSGLYPSLAGVGEQQGGGTTPRGAEQPRAEPGHAGLAPGPA
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GIPSPISEGDFKGYVSDNCTTLEPHRLVSRGIPGGPENSTTLTYQKVSCLLLKLNVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="envelope glycopolyprotein"
protein_id="AAC08989.1"
db_xref="G1:3003003"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_id="AAC08987.
ib_xref="G1:3003001"
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6309. .6617
/gene="env"
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1836. .2129
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/gene="env"
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'qene="env"
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/note="R"
22. .101
/note="U5"
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                                                                                                                                                                                                                                                                                                  /protein_id="AAA42546.1"
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GLVVILLLVVCLFCLLQCVSSSIRKMIDNSLGYREEYKKITGGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          829 IGAGTIAGCAACAIGCCITATAAGGAGAAAAAGCACCGIGCAIGCCGAITIGGIGGGAG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 TAAGGIGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAGGCAACAGACGGGTCTAAC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 ACGGATTGGACGAACCACTGAATTCCGCATTGCAGAGATATTGTATTTAAGTGCCCAGCT 438
J. Virol. 49 (2), 557-565 (1984)
84115081
6319755
Original source text: Rous-associated virus-2 covalently closed circular DNA, clone lambda-RAV2-2.
Location/Qualifiers
1. 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               949 ACGGATTGGACGAACCACTGAATTCCGCATTGCAGAGATATTGTATTTAAGTGCCTAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 CGATACAATAAACGCCATTTGACCATTCACCACATTGGTGTGCACCTGGGTTG 491
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Rous sarcoma virus strain Schmidt-Ruppin B, complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rous sarcoma virus Viruses; Retroviridae; Alpharetrovirus. Viruses; Retroid viruses; Retroviridae; Alpharetrovirus. 1 (bases 1 to 9396) Bouck, J., Skalka, A.M. and Katz, R.A. Complete nucleotide sequence of avian sarcoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.4%; Score 182; DB 14; Length 1560; Best Local Similarity 99.6%; Pred. No. 2.78-99; Matches 232; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="c in one clone; t in another clone"
099
                                                                                                                                                            /organism="Rous-associated virus type 2"
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Bouck, J., Skalka, A.M. and Katz, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   022. .>1560
product="viral mRNA"
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bp upstream of SphI site.
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'note="LTR'
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ALELTR2

346 bp ss-RNA linear VRL 28-APR-1993
Rous-associated virus 2 (RAV-2) LTR with reverse transcriptase endonuclease cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                           Duyk, G., Leis, J., Longiaru, M. and Skalka, A.M.
Selective cleavage in the avian retroviral long terminal repeat
sequence by the endomuclease associated with the alpha beta form of
avian reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Original source text: Rous-associated virus 2 replication form I DNA, clone RAV2-2 [1], and plasmids pPG1 and pGJ14 [2].

Reverse transcriptage associated endonuclease (purified from avian sarcoma virus) cleavage sites have been mapped in two trandemly linked Rous-associated virus-2 LTR sequences. The enzyme may be involved in viral cDNA integration in the host, since it generates a 6 bp staggered overlap that spans the junction. The clone sequence (RAV2-2) corresponds to the unintegrated replicative form (RF) I of RAV-2.

Draft entry for [2] kindly provided by A. Skalka, 15-AUG-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 TGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGGAG 318
                                                                                                                                                                                                                                            cleavage site; endonuclease cleavage site; long terminal repeat (LTR); reverse transcriptase endonuclease cleavage site. Rous-associated virus type 2 Rous-associated virus type 2
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Skalka,A.M., Duyk,G., Longiaru,M., DeHaseth,P., Terry,R. and
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1 (bases 1 to 346)
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Cold Spring Harb. Symp. Quant. Biol. 49, 651-659 (1984)
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    346
/organism="Rous-associated virus type 2"

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/note="rt-endonucleage cleavage site"
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/note="rt-endonuclease secondary
complement(244. .245)
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/note="rt-endonuclease
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/note="ltr B"
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RGLGPLQI WQTDFTLEPRNAPRSWLAVTVOTASSALVYQGGKYTSVARAGHWATAIA
VLGRFKAI KTDNGSCFTSKTREWLARWGIAHTTGI GONSQGQAWVERANRLLKDKIR
VLABGDGFRYKI IPASKQELLAKANYALNHPRRGENTKTPVQKHWRPTVLTEGEPPVKI
RIETGEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDITQKDEVTKKDEASPL
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FYERSRSGTWATEPKLFGDFNTSDTVTSPQRAGALAGGVTTFVALVDYBSWIETDLSF
KKGERLQIVNNTEGNWALHSVTTGCTGYIPSNYVAPSDSIQAEWYFGKLTRRESER
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VGQVLEPLRLKHPSLRMLHYMDDLLLAASSHDGLEAAGEEVINTLERAGFTISPDKIQ
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YEQLRGSDDNEARBNNLDMKMAMRIVQLSTTAALERWDPALPLGAVVRCEGGAIGY
LGQGLSTHPRCLWLFSTQPTKAFTAMLEVLTLITKLRASAVRTFGKEVDILLLPRC
FREDI PLPEGILLALRGFAGKIRSSDTPSIFDIARPLHVSLKYNTDHPVPGPTYFTD
ASSSTHKGVVVWREGPRWEIKEIADLGASVQQLEARAVAMALLLMPTTPTNVYTDSAP
VAKMLLKMGQEGVPSTAAAFILEDALSQRSAMAAVLHVRSHSEVPGFFTEGNDVADSQ
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protein_id="AAC08990.1"
db_xref="GI:3003004"
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9131. .9375
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                         /gene="gag"
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|gene="src"
|codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GACTITCCTACTIGGCAGTACATCTACGTAITAGTCATCGCTATTACCAIGGIGAIGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1999 JP 2000540258
16-JAN-1998 US 60/071673
DONNA ARMENTANO, NELSON YEW, JOHN MARSHALL
C12N15/09, AGIKA5/76, AGIK49/00, C12N15/00
Novel promoter element for sustained gene expression FH Location/Qualifiers
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C12N15/09, A61X5/76, A61X48/00, C12N15/00
Novel promoter element for gustained gene expression FH
Location/Qualifiers
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JD 2002508974-A/1.
Cytomegalovirus
(Yctomegalovirus
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Novel promoter element for sustained gene expression.
BD136064
                                                                                                                                                                                                          expression
                   no RNA stage; Herpesviridae;
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larity 100.0%; Pred. No. 1.4e-65;
Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Location/Qualifiers
                                                                                             1 (bases 1 to 282)
Armentano, D., Yew, N. and Marshall, J.
Novel promoter element for sustained gene
Patent: JP 2002508974-A 2 26-MAR-2002;
GENZYME CORP
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/organisme="Cytomegalovirus"
/mol_type="genomic DNA"
/do_xref="taxon:10358"
1 65 c 72 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cytomegalovirus"
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JP 2002508974-A/1
26-MAR-2002
15-JAN-1999 US 60/071673
         Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                     Cytomegalovirus
JP 2002508974-A/2
26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACCCCA 153
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Best Local Similarity
Matches 127; Conserv
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ORIGIN
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BD136064
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207 TGAGTTAGCAACATGCCTTATAAGGAGAAAAAAGCACCGTGCATGCCGATTGGTGGAAG 266
                                                                                                                                                                                                                   267 TAAGGTGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAGGGAACAGACGGGCTCTAAC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                         319 TAAGGIGGTATGATCGTGGTATGATCGTGCCTTGTTAGGAAGGCAACAGACGGGTCTAAC 378
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16-JAN-1998 US 60/071673
DONNA ARMENTANO, NELSON YEW, JOHN MARSHALL
C12N15/09, A61X5/76, A61X48/00, C12N15/00
Novel promoter element for sustained gene expression FH
Location/Qualifiers
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Novel promoter element for sustained gene expression.
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Novel promoter element for sustained gene expression.
BD136065
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Location/Qualifiers
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Armentano, D., Yew, N. and Marshall, J.
Novel promoter element for sustained g
Patent: JP 2002508974-A 3 26-MAR-2002;
GENZYME CORP
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/organism="Cytomegalovirus"
/mol_type="genomic DNA"
/db_xref="taxon:10358"
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Viruses; dsDNA viruses,
Betaherpesvirinae.
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JP 2002508974-A/3.
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JP 2002508974-A/3
26-MAR-2002
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Best Local Similarity 100.0
Matches 127; Conservative
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BD136065
LOCUS
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BASE COUNT ORIGIN

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          LOCUS
DEFINITION
ACCESSION
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SOURCE
ORGANISM
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AX360741
LOCUS
DEFINITION
ACCESSION
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VERSION
COUNCE
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                                                                                                                                                                                                                                                                                                     source
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ORIGIN
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AUTHORS
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JOURNAL
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AUTHORS
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                                                                                                                                 TITIGGCAGIACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                             317 TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 376
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                                                                        Gape
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C12N15/09, C07K14/61, C12N1/13, C12P21/02, C12N15/00 CC
Key
                                                  Length 512;
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
                                                Score 127; DB 6; I
Pred. No. 1.4e-65;
                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 590)
Hawkins, R. and Nakamura, M.
Signal peptide
Patent: JP 200054490-A 3 26-DEC-2000;
TOYOTA MOTOR CORP
                                                                                                                                                                                                                                                                                                                                                                                cauliflower mosaic virus promoter JP 2000354490-A/3 26-DEC-2000
                   132 t
                                                 Ouery Match 25.4%; Score 127; DB Best Local Similarity 100.0%; Pred. No. 1.44 Matches 127; Conservative 0; Mismatches
/mol_type="genomic DNA"
/db_xref="taxon:10359"
131 c 123 g 13
                                                                                                                                                                                                                                              590 bp
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JP 2000354490-A/3.
unidentified
unidentified
                                                                                                                                                                                                                                                        Signal peptide.
E59416
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                                                                                                                                                                                           CACCCCA 383
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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E59416
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ES1990 SPO DNA linear PAT 13-AUG-2002 Promoter, recombinant containing the same and utilization thereof. ES1990
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C12N15/09, A61K31/00, A61K31/00, A61K39/02, A61K39/17, A61K39/215,
C07K14/125,
C07K14/165, C07K14/30, C12N1/00, C12N15/00
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
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                                                                                 E51990.1 GI:18629551

E51990.1 GI:18629551

Human herpesvirus 5

Human herpesvirus 5

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.

I (bases 1 to 599)

Kubomura,M. and Saito,S.

Promocer, recombinant containing the same and utilizati
Patent: JP 201000188-A 5 09-JAN-2001;

NIPPON ZEON CORP.
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/organism='Cytomegalovirus'.
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
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/organism="Human herpesvirus 5"
/mol_type="genomic DNA"
/db_xref="taxon:10359"
114 c 144 g 159 t
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CORIXA CORPORATION (US)
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Seguence 425 from Patent WO0202623.
AX360741
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JP 2001000188-A/5
09-JAN-2001
22-JUN-1999 JP 1999174804
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bunoul45 11-JAN-2002 Vector having stabilized sequence and eucaryotic host cell.
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/ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Vector having stabilized sequence and eucaryotic host cell
Patent: JP 2000308497-A 3 07-NOV-2000;

GENERAL INC INC
OS Unidentified
PN JP 2000308497-A/3
PD 07-NOV-2000
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                                               restriction
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                              Lin, J., Yaver, D., Foster, D. and Holly, R.
Methods for expressing endogenous genes by re
mediated integration
Patent: WO 0236760-A 24 10-MAY-2002;
Novozymes Biotech, Inc. (US); ZymoGenetics,
Location/Qualifiers
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12-SEP-1986 US 907185,09-JUL-1987
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PN JP 200308497-A/3
PD 7-NOV-200308497-A/3
PF 17-ARX-2000 JP 2000115248
PR 12-SEP-1986 US 907185,09-JUL-198
CORNELLIA MAXIN GOMAN
CC C C 12N15/09,C12N5/10,C12N15/00,C12N5/00
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                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
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1 (bases 1 to 777)
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BD000145
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AUTHORS
TITLE
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                   REFERENCE
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Bodysone receptor-based inducible gene expression system
Patent: WO 0170816-A 60 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
Location/Qualifiers
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                                                                                               Query Match
25.4%; Score 127; DB 6, I
Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
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Pred. No. 1.4e-65;
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/organism="synthetic construct"
/mol_type="qenomic DNA"
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100.0%; Pred. No....
0; Mismatches
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Sequence 24 from Patent W00236760.
AX591955
AX591955.1 GI:27950185
                                                                                                                                                                                                                                                                                                                                                                                                                  AX256412 619 bp
Sequence 60 from Patent W00170B16.
AX256412
AX256412.1 GI:16075237
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               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
152 c 141 g 15
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synthetic construct
artificial sequences.
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Best Local Similarity 100.0
Matches 127; Conservative
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AX591955
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AX256412
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VRL 02-AUG-1993

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343 GACTITCCTACTIGGCAGIACATCTACGIAITAGTCATGGCTATTACCATGGTGATGCGG 402
                                                                             403 TITTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 462
                                                  77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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Lehner,R., Stamminger,T. and Mach,M.
Comparative sequence analysis of human cytomegalovirus strains
9.129918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Human herpesvirus 5"
/mol_type="genomic DNA"
/db_xref="taxon:10359"
/cell_line="infected human foreskin fibroblast"
209 c 201 g 238 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.4%; Score 127; DB 14; Length 875; Best Local Similarity 100.0%; Pred. No. 1.4e-65; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     enhancer region, promoter region.

Human herpesvirus 5

Human herpesvirus 5

Human herpesvirus 5

Human herpesvirus 5

Human herpesvirus 6

Betaherpesvirinae, Cytomegalovirus
                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Original source text: Human cytomegalovirus DNA.
individual isolate: patient G.A.
major immediate early gene enhancer.
Location/Qualifiers
1. .875
                                                                                                                                                                                                                                         HS5PIE1AB 875 bp DNA
Human cytomegalovirus IE-1 promoter region.
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ORIGIN
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HSSPIELAB
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                  136
                                      TITIGECAGTACATCAATGGGGGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 462
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Gorman.C.M.
A transient expression system for producing recombinant protein Patent: EP 0309237-Al 3 29-MAR-1989;
Location/Qualifiers
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25.4%; Score 127; DB 6; Length 777;
Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 127; Conservative 0; Mismatches 0;
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Location/Qualifiers
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105430
105430.1 GI:591075
                TTTTGGCAGTACATCAATGGGCGTGGATAGCGG
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Sequence 3 from Patent EP 0309237.
108105
108105.1 GI:589184
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188 a 205 c 190 g
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205 c 190 g
                                                                                                                                                                                                                                                                                                           Unknown.
Unclassified.
1 (bases 1 to 777)
Gorman, C.M.
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TITLE
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I05430
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AUTHORS
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S2 subtraction lib
Cytomegalovirus (C
Human cytomegalovi
Cauliflower mosaic
Cytomegalovirus (C
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                                                                                                                                                                                    February 15, 2004, 19:07:11; Search time 161.871 Seconds (without alignments) 8338.264 Million cell updates/sec
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/SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:
/SIDS1/gcgdata/geneseq/
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| SIDS1/goddata/geneseqn/geneseqn-embl/NA1981.DAT:
| SIDS1/goddata/geneseqn/geneseqn-embl/NA1981.DAT:
| SIDS1/goddata/geneseq/geneseqn-embl/NA1984 DAT:
| SIDS1/goddata/geneseq/geneseqn-embl/NA1984.DAT:
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Human lung tumour Cauliflower mosiac	CMV promoter / mou	Cytomegalovirus de	al expres	DNA sequence of po	ξ	Partial expression	DNA sequence of po	Enhancer for eukar	HCMV (AD169) major	Sequence of HCMV(A	HCMV immediate ear	Adeno-associated v	Human Sonic hedgeh	o	Human Shh gene PCR	Human Sonic hedgeh	Human Shh gene and	Human sonic hedgeh	Nucleotide sequenc	Human Sonic hedgeh	Plasmid CMV-delRT	DNA encoding CTLA-	CMV-PC-PSA promote	CMV-PSA promoter.	DNA encoding Synec	CMV promoter / mou	Chimeric sequence		Wild-type human AD	Human ovarian anti	Transgenic APP DNA	Reporter gene cons	DNA encoding N-ter	Promoter-enhancer	CMVintA promoter a
ABK16313 AAS15664	4	AAZ95643	AAN82445	AAN90697	~	AAN81527	AAN90695	AAN60156	AAQ53550	AAQ43524	AAT77193	AAD37261	AAX25629	AAX25113	AAX16193	AAA27888	AAA30286	AA166796	AAH28445	AAD23811	AAV58058	AAV03231	AAT29597	AAT29595	ABX04557	AAL44408	AAL38382	AAL38380	339	O	AAZ89475	AAA47118	ABX04567	AAN91042	AAQ74211
24	24	21	σ	10	25	σ	10	7	14	14	18	24	20	20	20	21	21	22	22	24	19	19	17	17	23	24	24	24	54	54	21	21	23	20	15
619	738	763	777	777	884	919	919	930	930	930	930	987	966	966	966	966	966	966	966	966	1070	1104	1215	1216	1467	1632	1715	1767	1767	1787	1813	1814	2043	2133	2196
25.4	25.4	S	S	LO.	S	S	25.4	S	S	25.4	ហ	25.4	25.4	ហ	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	'n	25.4	25.4	'n	'n.	'n	'n.	'n.	'n.	ın	'n.	'n.	ın.
127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127
6 0	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42		44	

ALIGNMENTS

Human, vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1; chronic limb ischaemia; myocardial ischaemia, autoimmune disorder; pHE4a; albragic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferative disorder; viral infection; bacterial infection; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; gene therapy. Expression vector construct pVGI.1 containing VEGF-2 insert. BP. ABK10062 standard; DNA; 5283 03-AUG-2001; 2001WO-US24658; 04-AUG-2000; 2000US-223276P. (first entry) WO200211769-A1. 21-MAY-2002 14-FEB-2002. Synthetic. ABK10062; ABK10062

(HUMA-) HUMAN GENOME SCI INC.

Coleman TA;

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Cytomegalovirus-derived promoter element-2; CMV-derived promoter element; cytomegalovirus immediate early promoter; human alpha-galactosidase gene; persistent transgene expression; expression cassette; human CFTR gene; human cystic fibrosis transmembrane conductance regulator gene; adenoviral vector; E4 region; transgene; plasmid; ds.
                             Cytomegalovirus-derived promoter element-2 (-299
19-OCT-1999 (first entry)
                                                                                                                                              Cytomegalovirus.
                                                                                                                                                                          Key
promoter
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                                                                                                                                        expression vector construct containing the vacular endothelial growth factor 2 (VBGF-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell with the DNA and for treating a patient having chronic limb ischaemia or myocardial ischaemia, or a disease or disorder selected from autoimmune disorders (e.g. rheumatorid arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease), diseases due to viral, bacterial, fungal or parasitic infection, cardiovascular disorders (e.g. cardiowascular disorders (e.g. cardiowascular disorders and embolism. This sequence represents the pVGI.1 expression vector containing the VBGF-2
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                           Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischaemia or myocardial ischaemia, autoimmune disorders and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCATGGTGATGCGGTTTTTGGCAGTACATCGGCGTGGATAGCGGTTTGACTCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGGCGTGGATAGCGGTTTGACTCACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGCTTGACCTTATGCGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT
                                                                                                                             The invention relates to an isolated nucleic acid comprising pVGI.1
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                                                                                                                                                                                                                                                                                                                                                     Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             IndelB
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 500; DB 24;
100.0%; Pred. No. 4.1e-262;
Live 0; Mismatches 0;
                                                                                                   Disclosure, Fig 31; 241pp; English.
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WPI; 2002-217153/27
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The present sequence is a promoter element derived from the cytomegalovirus (CWV) immediate early promoter. The promoter the promoter element is used to achieve persistent expression of an operably linked transgene, especially human cystic fibrosis transmembrane conductance regulator especially human cystic fibrosis transmembrane conductance regulator expression of the man alpha-galactostidase gene, in a target cell. The expression cassette comprising the promoter element operably linked to a transgene is delivered to a target cell via a plasmid or an adenoviral vector lacking the B4 region. As the promoter element functions independently of the viral E4 region, this allows the use of vectors containing reduced viral genomes thereby increasing the carrying capacity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing reduced viral genomes thereby increasing the carrying capacity of the vector while decreasing the potential for host immune reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytomegalovirus (CMV)-derived promoter element and human albumin one enhancer elements useful for persistent gene expression
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                                                               a
CMV_derived_promoter_element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 281 BP; 67 A; 64 C; 73 G; 77 T; 0 other;
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Location/Qualifiers
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Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marshall
                                                                                                                                                                                                                                                                                                                                                                                         (GENZ ) GENZYME CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Armentano D,
                                                                                                                                                                                                                                                                                                                                16-JAN-1998;
                                                                                                                                                  WO9936557-A1
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AAX80726
ID AAX8
XX
AC AAX8
XX
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AAX80727 standard; DNA; 281

AAX80727

RESULT 2
AAX80727
ID AAX8
XX
AC AAX8

Key

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ABD17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and ABP54446 to ABB54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, incrobiology, molecular biology and recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 TITITGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 434
                                                                                               Human, cancer, tumour, therapy, diagnosis, CT antigen, CP antigen,
immune response, virology, immunology, microbiology; molecular biology,
recombinant DNA technology, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 GACTITICCTACTIGGCAGIACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic polynuclectides or polypeptides useful for diagnosing preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGCTGGTGTGCG
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                                                       $2 subtraction library cancer related clone SEQ ID NO:412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 481 BP; 121 A; 119 C; 109 G; 132 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaiger A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 412; 207pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang S, Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001US-280255P.
28-AUG-2001; 2001US-315563P.
09-JAN-2002; 2002US-347313P.
                                                                                                                                                                                                                                                                                                                                         28-MAR-2002; 2002WO-US10421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in virology, immunology, mi
recombinant DNA techniques
       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-058387/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                            WO200278516-A2.
                                                                                                                                                                                              Homo sapiens
          23-JAN-2003
                                                                                                                                                                                                                                                                                           10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a promoter element derived from the cytomegalovirus (CMV) immediate early promoter. The promoter element is used to achieve persistent expression of an operably linked transgene, especially human cystic fibrosis transmembrane conductance regulator gene (CFTR gene) or human alpha-galactosidase gene, in a target cell. The stransgene is delivered to a target cell via a plasmid or an adenoviral transgene is delivered to a target cell via a plasmid or an adenoviral independently of the viral E4 region. As the promoter element functions independently of the viral E4 region, this allows the use of vectors containing reduced viral genomes thereby increasing the carrying capacity of the vector while decreasing the potential for host immune reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                       Cytomegalovirus-derived promoter element-1; CMV-derived promoter element; cytomegalovirus immediate early promoter; human alpha-galactosidase gene; persistent transgene expression; expression cassette; human CFTR gene; human cystic fibrosis transmembrane conductance regulator gene; adenoviral vector; E4 region; transgene; plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 TITTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGGATTTCCAAGTCTC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GACTITICITACITIGGCAGTACAICITACGIATITAGICATCACCATGGIGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A cytomegalovirus (CMV)-derived promoter element and human albumin gene enhancer elements useful for persistent gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 127; DB 20; Length 282;
100.0%; Pred. No. 8.1e-59;
tive 0; Mismatches 0; Indels
                                               Cytomegalovirus-derived promoter element-1 (-295 to -14).
                                                                                                                                                                                                                                                                                                        1..282
/*tag= a
/label= CMV_derived_promoter_element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 282 BP; 68 A; 65 C; 72 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Pages 48-49; 56pp; English.
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yew N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ17986 standard; cDNA; 481 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US00915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0071673
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 CACCCCA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-478911/40.
                                                                                                                                                                                                                                       Cytomegalovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1999;
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  19-0CT-1999
                                                                                                                                                                                                                                                                                                             promoter
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Gaps ;

Best Loca Matches

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ABZ17986
ID ABZ1
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AC ABZ1

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administered to a patient having a disease associated with an aberrant

Seguence 500 BP; 121 A; 126 C; 125 G; 128 T; 0 other;

form of the gene.

88333

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Gaps

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Length 500; 0; Indels

Score 127; DB 19; Pred. No. 8e-59; 0; Mismatches 0;

25.4%; Scc. 100.0%; Pre

Matches 127; Conservative

Similarity

Query Match Best Local

290

231 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG

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17 GACTITICCIACTIGGCAGIACAICIACGIAITAGICAICGCTAITACCAIGGIGAIGCGG

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DNA containing inactive, mutated binding site for Gfi-1
transcription repressor - used to increase gene expression in vitro
               transcription repressor; mutation; cytokine; gene therapy; factor independence-1; cytomegalovirus; promoter; ss.
Cytomegalovirus (CMV)-MIE wild-type promoter sequence.
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*tag= e
note= "putative Gfi-1 binding site"
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note= "putative Gfi-1 binding site"
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                                                   Location/Qualifiers
331..342
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                                                                                                                                                                                                                                                                                                                                                                                                             anscription repressor - used to
in vivo, e.g. in gene therapy
                                                                                                                                                                                                                                                                                                                                                       (FOXC-) FOX CHASE CANCER CENT.
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                                      Human cytomegalovirus
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                                                            misc binding
                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                   TATA_signal
                                                                                                                                                                                                                                                   CAAT_signal
                                                                                                                                                                                                                                                                                                                                                                      Grimes HL,
                      growth
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77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                291 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the Human cytomegalovirus promoter region. The compositions of the invention bind to this sequence. The specification describes a composition that comprises low density lipoprotein (LDL) and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or riboxyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and
                                                                                                                                                                                                                                                                                                                       apolipoprotein; binding; in vivo transport; nucleic:acid; binding dom:
nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
non-small cell lung carcinoma; diabetes; arteriosclerosis;
Human cytomegalovirus promoter region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 589 BP; 157 A; 140 C; 143 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                         Human cytomegalovirus promoter region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 74; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                       5163/c
AAX15163 standard; DNA; 589 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0079030
97US-0874807
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                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus
                                                                  143
                                                                                                   351 CACCCCA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-070331/06.
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                                                                  CACCCCA
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                                                                                                                                                                                                                        AAX15163;
                                                                                                                                                                   AAX15163,
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This is the wild-type cytomegalovirus (CWV)-MIE promoter sequence comprising two putative Gfi-1 (growth factor independence-1) transcription repressor binding sites. This promoter can be mutated at the Gfi-1 binding sites to be used in a novel isolated DNA construct which contains at least one mutated binding site for a Gfi-1 to transcription repressor that hinders or prevents binding of Gfi-1 to this site. The expression vector contains an expression regulatory segment that contains at least one copy of the sequences shown in AAV19671 to AAV19685 linked operably to a coding segment selected from a group of cytokines, interleavins, interferons, growth factors and protonocogenes, and an isolated DNA molecule containing one of two 500 base increases expression of these genes controlled by regulators that include binding sites for Gfi-1 both in cultured cells and in vivo (for gene therapy or DNA vaccination). A vector containing a normal gene under control of a regulator with the mutated binding site can be

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The invention relates to a 5' and a 3' fragment of the chicken beta-actin promoter (AAPS4422 and AAPS4413), respectively), which exhibit promoter activity. The chicken beta-actin promoter fragments may be used to drive expression of a heterologous gene in a recombinant vector used as the active component of a genetic vaccine. The present sequence represents a cytomegalovinus (GWV) immediate-early (IE) promoter aniancer, a portion of which was used in the construction of the chimeric Pec promoter (AAF84454) in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
               374 TriricecaGracarcarcargesceregaraecegriricaecrcaceeegarrrcaagrere 433
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                                                                                                                                                                                                                                                                 Cytomegalovirus (CMV) immediate-early (IE) promoter enhancer
                                                                                                                                                                                                                                                                                               Cytomegalovirus; CMV; immediate-early; IE promoter enhancer; Pec promoter; chicken beta-actin promoter; recombinant vector; genetic vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 127; DB 22; Length 599; 100.0%; Pred. No. 8e-59; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA molecule for use as a promoter for preparing a recontaining the DNA which is used for preparing a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 599 BP; 152 A; 144 C; 144 G; 159 T; 0 other;
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                                                                                                                                                                  AAF84456 standard; DNA; 599
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                                                                                                                                                                                                                                                                                                                                                                   Human cytomegalovirus
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                                                 137 CACCCCA 143
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ID AAF8
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ID ABK1
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                                                                                                                            77 ITTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                                   216 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 157
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X 2 = Gly-Ser-Leu or Pro-Leu-Ala,
The signal peptides are useful in the preparation of human growth
hormone and transformed chlorella. Signal peptides, DNA encoding the
hormone expression cassettes, recombinant vectors containing the
cassettes, and transformants having the vectors are provided. The
present sequence is a promoter which may be used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal peptides useful for the preparation of human growth hormone transformed chlorella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is provided in a specification relating to signal peptides for expression and secretion of a protein in chlorella. The peptides are of the formula:

Met-Ala-Asn-Lyg-X_1-(Leu)_n-X_2-Ala-Ser-Gly.
                                                                17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTALTACCATGGTGATGCGG
                                                                                              276 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cauliflower mosaic virus; promoter; signal peptide; chlorella; gene expression; protein production; human growth hormone; ds.
25.4%; Score 127; DB 20; Length 589; 100.0%; Pred. No. 8e-59; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.4%; Score 127; DB 22; Length 590; Best Local Similarity 100.0%; Pred. No. 8e-59; Matches 127; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 590 BP; 149 A; 143 C; 141 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 12; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                Cauliflower mosaic virus promoter,
                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                  590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0168271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0168271,
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TOYT ) TOYOTA JIDOSHA KK.
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                AAH24425 standard; DNA;
                                                                                                                                                                                                CACCCCA 143
                                                                                                                                                                                                                                CACCCCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-275809/29.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    = Ser or Leu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2000354490-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000,
                                 127;
                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                                                                                AAH24425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                   Best Loca
Matches
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gene expression systems useful for modulating gene expression in host cells. The gene expression system encodes a polypeptide with a DNA-binding domain recognizes a response element associated with a gene whose expression is to be modulated and/or a ligand binding domain (IBD) comprising a IBD from a nuclear receptor and a second gene expression cassette capable of being expressed in a host cell comprising a transpolymucleotide sequence encoding escond polypeptide comprising a transpolymucleotide sequence encoding second polypeptide comprising a transpolymucleotide sequence encoding second polypeptide comprising a transpolymuclear receptor other than an ecdysone receptor, a retinoid X receptor of the TADP (USP) (the transactivation domain is from a nuclear receptor other than an ecdysone receptor, a retinoid X receptor or a USP receptor and the IBDPs from the first and second polypeptides are different and dimerise). The ecdysone and retinoid X receptor based inducible gene expression systems useful for modulating gene expression proteins and antibodies, cell-based high-throughput screening assays (HTS), functional genomic and regulation of traits in transgenic plants and animals. The present sequence represents a cauliflower mosiac virus, CWV, promoter which is used in an inducible gene expression as ystem of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Ecdysone and retinoid X receptor based inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 373
                       transactivation domain; nuclear receptor; ultraspiracle; gene therapy; protein production; antibody production; high throughput screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 GACTITICOTACTIGGCAGIACATCIACGIATIAGICATCGCTATIACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTGGCAGTACATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                         Ecdysone and retinoid X receptor based inducible gene expression systems for use in e.g. gene therapy, large scale production of proteins and cell-based high-throughput screening assays -
     CMV promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 127; DB 22; Length 619;
Pred. No. 8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 619 BP; 150 A; 164 C; 155 G; 150 T; 0 other;
       retinoid X receptor; RXRalpha; DNA-binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                          HTS; transgenic plant; transgenic animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 140-141; 144pp; English
                                                                                                                                                                                                                                                                                                                                    Cress DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL44414 standard; DNA; 738 BP
                                                                                                                                                                                                       21-MAR-2001; 2001WO-US09050
                                                                                                                                                                                                                                          22-MAR-2000; 2000US-191355P.
20-FEB-2001; 2001US-269799P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%;
                                                                                                                                                                                                                                                                                                                                    Kapitskaya MZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Lov.
Matches 127; Conservative
                                                                                           Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                               (ROHM ) ROHM & HAAS CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656841/75.
                                                                                                                                WO200170816-A2
                                                                                                                                                                    27-SEP-2001,
                                                                                                                                                                                                                                                                                                                                  Palli SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides. Compositions comprising the lung tumour polypeptides, polypeptides, fusion proteins, antibodies to the polypeptides, T cell populations, or antigen presenting cells that express the lung tumour polypeptides, are useful for treating lung cancer or stimulating an immune response. The polymucleotides and polypeptides are also useful in the diagnosis and monitoring of lung cancer. Sequences ABK15889-AAS16343 represent CDNA molecules encoding the polypeptides of the invention and PCR primers used to amplify the CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTITICCIACTIGGCAGIACAICIACGIATIAGICATCGCIATIACCAIGGTGAIGCGG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGGCAGTACATCCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 397
                                                                                                          Human; lung tumour protein; lung cancer; immunostimulant; cytostatic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymucleotides encoding lung tumour polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTITCCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides encoding lung tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                            Henderson RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.4%; Score 127; DB 24; Length 600; 100.0%; Pred. No. 8e-59; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 600 BP; 153 A; 152 C; 141 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecdysone receptor; EcR; ligand binding domain; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter D,
                                                                   Human lung tumour protein encoding cDNA #425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 261-262; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            Wantanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cauliflower mosiac virus promoter,
                                                                                                                                                                                                                                                                                                        29-JUN-2000; 2000US-215696P.
22-AUG-2000; 2000US-227142P.
06-SEP-2000; 2000US-230481P.
21-DEC-2000; 2000US-257729P.
                                                                                                                                                                                                                                                                       28-JUN-2001; 2001WO-US20975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS15664 standard; DNA; 619
                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcneill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
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                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                  WO200202623-A2.
                                                                                                                                                                 Homo sapiens.
                                    14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2002
                                                                                                                                                                                                                                      10-JAN-2002
                                                                                                                            primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS15664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T,
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(first entry)

08-JUN-2000

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The method involves introducing a restriction enzyme and a nucleic acid regulatory sequence into mammalian cells - for integrating the nucleic acid construct into the mammalian cell genome at sites generated by the restriction enzyme. Mutant mammalian cells having a trait of interest can then be selected. The method of the invention is useful for isolating a gene controlling a trait of interest from a mammalian cell. The method is useful for discovering and isolating new genes. The method of the invention can be used to create large libraries of mammalian cells which have a low transfection efficiency. The method of the invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 gacitirectactificacagracarcracgratragreardectarraceargergarges 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 irriredekárhacarcaardageegrekarhadegerrireacreacagagarrireakagrere 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           poorly. The present DNA sequence represents a chimeric gene sequence comprising a Cytomegalovirus (CMV) promoter and a murine G-CSF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suitable for over-expressing a known endogenous gene that is expressed poorly. The present DNA sequence represents a chimeric gene sequence
                                                          CMV promoter / mouse G-CSF receptor, (G-CSFR) gene 9 - chimeric sequenc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 ITTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises a method for producing a mutant mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of a mutant mammalian cell for isolating genes, comprising integrating a nucleic acid construct into the cell genome at sites generated by the restriction enzyme, and selecting cell with trait of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                          Mouse; murine; ds; gene of interest isolation; CMV; gene; promoter; novel gene discovery; novel gene isolation; large library production; G-CSF receptor; G-CSFR; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 738 BP; 188 A; 178 C; 168 G; 204 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; Fig 14; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVOZYMES BIOTECH INC (ZYMO ) ZYMOGENETICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ95643 standard; DNA; 763
                                                                                                                                                                                                                                                                                                                         30-OCT-2001; 2001WO-US45045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin J, Yaver D, Foster D,
                                                                                                                                                                                                                                                                                                                                                                  30-OCT-2000; 2000US-0702177
                                                                                                                                                                                 Chimeric - Mus sp.
Chimeric - Cytomegalovirus.
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCCCA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-566503/60.
                                                                                                                                                                                                                                           WO200236760-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention
                                                                                                                                                                                                                                                                                    10-MAY-2002.
                   31-OCT-2002
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AAZ95643
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Holly R;

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A method has been developed of increasing prostanoid production in vivo comprising delivering and hyperexpressing a prostaglandin synthase gene in calls. The method can be used for gene therapy. The method is useful for the treatment of diseases such as pulmonary embolus, myocardial infarction and general lung disease (e.g. adult respiratory distress syndrome). Generally the present invention provides a plasmid comprising a cytomegalovirus (GWV) derived promoter sequence driving the coding region for ovinine prostaglandin G/H synthase (PGH). In order to increase translation augmenting sequence and a portion of the 3' untranslated region from the human growth hormone (hGH) gene. The present sequence represents the CMV promoter sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGITIGACICACGGGGAITICCAAGICIC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 tringgcagracarcaargagcgragaragcggringacrcacgggarriccaagrcic 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GACTITCCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
for
                                                                                    ovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing prostanoid production in vivo comprising delivering hyperexpressing a prostaglandin synthase gene in cells, useful treating e.g. myocardial infarction and general lung disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.4%; Score 127; DB 21; Length 763; 100.0%; Pred. No. 8e-59; ive 0; Mismatches 0; Indels
                                                                            Cytomegalovirus, CMV; promoter; human growth hormone; PGH; prostaglandin G/H synthase; plasmid; prostanoid; circular; cardiant; thrombolytic; antiinflammatory; gene therapy; pulmonary embolus; myocardial infarction; lung disease; adult respiratory distress syndrome; ds.
                                                Cytomegalovirus derived promoter sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 763 BP; 203 A; 174 C; 164 G; 222 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conary JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 7-10; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Canonico A, Brigham K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.48;
                                                                                                                                                                                                                                                                                                                                   91US-0746941.
                                                                                                                                                                                                                                                                                                 95US-0459493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (UYVA-) UNIV VANDERBILT
                                                                                                                                                                                          Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCCCA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-205193/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                 02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                     19-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                      21-JUN-1993;
                                                                                                                                                                                                                              US6030638-A
                                                                                                                                                                                                                                                                29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                         Meyrick B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
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AAN82445
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Gaps

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Indels

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100.0%; Preu. ...

25.48;

Score 127; DB 24; Length 738; Pred. No. 8e-59;

16

136

AAN82445 standard; DNA; 777 BP

AAN82445;

SAKE

BB

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DNA sequence of portion of plasmid pF8CSSS containing the cytomegalovirus enhancer and promoter and an engineered stabilising.
                                                                                                                                                                                                                       /*tag= b honte="stabilising sequence including the engineered splice donor and acceptor sequence"
                                                                                                                                                                                                'note="cytomegalovirus enhancer, promoter and leader
                                                                                        Plasmid pF8CSSS; cytomegalovirus; SV40; enhancer; promoter; stabilising sequence; splice donor intron sequence; Ig region; splice acceptor sequence; human embryonic kidney cells (293);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transient expression system for recombinant proteins - comprising eukaryotic host cell transfected with vector encoding trans-activating protein and expression vector
                                                                                                                                                                                                                                                                                'note="remaining leader"
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /note="Begin RNA"
                                                                                                                                                                                                                                                                                                                                                                                                             87US-0101712.
                       (updated)
(first entry)
                                                                                                                                                                                                          733..736
                                                                                                                                                                                     /*tag=
                                                                                                                                      Cytomegalovirus, SV40.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-095394/13.
                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1987;
                      25-MAR-2003
15-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                29-MAR-1989
                                                                                                                                                                                                                                                                                                                                         EP309237-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorman CM;
 AAN90697;
                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                         misc_RNA
                                                                                                                                                                                                                                                                                            misc_RNA
                                                                                                                                                               Key
 343 GACTITICCIACTIGGCAGIACAICTACGIAITAGICAICGCTAITACCAIGGIGAIGGCGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGIIIGACICACGGGGAIITICCAAGICIC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 TITIGGCAGIACAICAAIGGGCGIGGAIAGCGGIIIGACICACGGGGAIIICCAAGICIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In the expression vectors of the invention, the promoter is specifically from the immediate early gene of human cytomegalovirus (CMV) or from simian virus (SV40). The stabilizing SQ contains 1 or 2 splice donor-intron-acceptor SQs, esp. from the specified CMV gene, or the intron is from CMV or the Ig variable region, while the splice-acceptor component corresponds to the Ig acceptor SQ. The vector may also include (upstream of the promoter) an enhancer, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                              Expression vector; promoter; heterologous protein; mammalian vector;
                                                                                                                                                                                                                                                                                                                                                                                                 Continuous expression of heterologous protein in eukaryotic cells - by transfecting with vector contg. stabilising sequence, promoter, structural gene, poly:adenylate sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 777 BP; 188 A; 205 C; 190 G; 194 T; 0 other;
                                                                                                                                     from pPMLCMV beginning tenhancers and promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.4%; Score 127; DB 9;
100.0%; Pred. No. 8e-59;
ative 0; Mismatches 0
                       expression vector pF8CSSS sequence.
                                                                                                                                                             612
/*tag= b
/note= "starts here"
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example, Fig 19, 48pp, English.
                                                                                                                               a
"from
                                                                                                                                                                                                                                                                              87US-0071674.
86US-0907185.
87US-0101712.
                                                                                                                                                                                                                                                         87EP-0308060
06-MAR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 127; Conservative
                                                                                                                           /*tag=
/note=
                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1988-072583/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                    termination site
                                                                               Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also from SV40
                                                                                                                 misc_feature
                                                                                                                                                                                                                                                         11-SEP-1987;
                                                                                                                                                                                                                                                                                            12-SEP-1986;
25-SEP-1987;
                                                                                                                                                                                                                                                                                39-JUL-1987;
                                                                                                                                                                                                                                 16-MAR-1988
                                                                                                                                                                                                           EP260148-A
                                                                                                                                                                                                                                                                                                                                                    Gorman CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                                                                                                                                               mRNA
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Expression vector pF8CSSS contains the cytomegalovirus enhancer and promoter, an engineered stabilising sequence, the cDNA encoding factor VIII and the SV40 polyadenylation site. The entire intron region including donor and acceptor sequences was deleted and replaced by an engineered stabilising sequence. PF8CSSS is used in amethod for prodn. Of a desired heterologous protein in a eukaryotic host cell. The method comprises: transfecting a eucaryotic host cell with a vector conding trans-activating protein; transfecting the host cell with a nexpression vector having a sequence of a ds DNA comprising, an expression vector having a sequence of the desired protein, and a DNA encoding the amino acid sequence of the desired protein, and a polyadenylation sequence upstream to a transcription termination site. The pref. host cells are human embryonic kidney cells (293) or JW2. The method provides useful quantities of a desired protein in a relatively short period of time without having to establish continuous prodn. The transient expression system optimises the interaction between specific vector components and certain trans-activating proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 777 BP; 188 A; 205 C; 190 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.4%; Score 127; DB 10;
100.0%; Pred. No. 8e-59;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Updated on 25-MAR-2003 to correct PN field.)
Disclosure; ; 44 pp.; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.4 Best Local Similarity 100. Matches 127; Conservative
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RESULT 14 AAN90697 ID AAN90697 standard; DNA; 777 BP. XX

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TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                   343 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 402
                                                                                                                                                                                                                  403 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZNPP)2 or ZNNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammanian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus crythematosus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMV enhancer/Myeloproliferative sarcoma virus LTR promoter construct DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZINF9; ZINF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; autoAmmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; cytomegalovirus; CWV; chimeric; gene; ds.
92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408..884
/*tag= b
/note= "Myeloproliferative sarcoma virus LTR promoter"
17 GACTITCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pransmembrane activator and calcium modulator and cyclophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Cytomegalovirus.
Chimeric - Myeloproliferative sarcoma virus.
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/note= "CMV enhancer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD53783 standard; DNA; 884 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..407
/*tag=
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                                                                                                                                                                                                                                                                                     137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                            463 CÁCCCA 469
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                                                                                                                                          17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
AAD53783
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116 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 375
                                                                                                                                                                                                                                                                                                                                                        256 gacifitéchactrescaracarchacgrafitagreatescratificatescaracardes 315
                                                                                                                                                                                                                                                                                                                                                                                                      77 TITIGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                                                                                                                                                                                             94
multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is Cytomegalovirus (CMV) enhancer/Myeloproliferative sarcoma virus LTR promoter construct DNA used in the invention.
                                                                                                                                                                                                                                                                                                             17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                  Length 884;
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                                                                                                                                                                       Sequence 884 BP; 229 A; 236 C; 214 G; 205 T; 0 other;
                                                                                                                                                                                                             25.4%; Score 127; DB 25;
100.0%; Pred. No. 7.9e-59;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 15, 2004, 22:40:23
Job time : 165.871 secs
                                                                                                                                                                                                                                                               Matches 127; Conservative
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                                                                                                                                                                                                                                           Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                             569978 segs, 220691566 residues
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500
                                                                                  OM nucleic - nucleic search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lssued_Patents_NA:*
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2: /cgT2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgT2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgT2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgT2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Post-processing: Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

		Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl	App1:	App11	Appl	Appl	Appl	Appl	Appl	Appli	App1i
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Description		Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
QI		-08-459-493-	-08-029	US-08-029-022-4	6-3	-08-246-376-	-07-972	-07-972-135-	-08-256		US-09-006-841-4	PCT-US93-05366-2	PCT-US93-05366-4	310-842-	-08-522-8	3-522-841-	US-09-310-842-3	-310-842	0-17	9-310-84	US-09-310-842-4	US-09-800-170-47	US-08-037-816A-13	US-08-530-146-13	US-09-340-798A-43	US-09-470-661A-32	US-08-801-092-5	US-09-315-113-5
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* Qu <i>ery</i> Match Length		763	930	930	930	930	930	930	930	930	930	930	930	1078	1215	1216	1318	1417	1467	164	187	2043	N	12	4	٢	85	ŧΩ .
% Query Match		25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4
S. 97		127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127
Result		н	7	r	4	υ	Q	7	80	σn	10	11	12	13	74	15	16	17	18	0 1	20	21	22	23	24	25	26	27

TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) ANTI-SENSE: NO FEATURE: NAME/KEY: promoter

Sequence 9, Appli Sequence 84, Appli Sequence 84, Appli Sequence 19, Appli Sequence 19, Appli Sequence 4, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 28, Appli Sequence 28, Appli Sequence 33, Appli Sequence 34, Appli Sequence 34, Appli Sequence 37, Appli			
28 127 25.4 3925 3 U3-09-011-745-9 29 127 25.4 3944 1 U3-07-678-408A-1 30 127 25.4 3987 4 U3-07-68-649B-83 31 127 25.4 4026 3 U3-08-649B-83 33 127 25.4 4026 3 U3-08-25-15-113-19 34 127 25.4 4059 2 U3-08-25-493C-4 35 127 25.4 4059 3 U3-08-25-493C-4 36 127 25.4 4059 3 U3-08-25-493C-4 38 127 25.4 4059 5 PCT-U395-07554-4 39 127 25.4 4059 5 PCT-U395-07554-4 39 127 25.4 4069 4 U3-09-170-496D-288 41 127 25.4 4069 4 U3-09-170-456D-287 42 127 25.4 4059 3 U3-08-010-23-8 43 127 25.4 4059 4 U3-09-170-415-3 43 127 25.4 4069 4 U3-09-170-315-4 42 127 25.4 4059 103-09-170-315-4 42 127 25.4 4069 4 U3-09-170-315-4 42 127 25.4 4249 3 U3-08-010-032-3 43 127 25.4 4249 3 U3-08-010-032-3 44 127 25.4 4283 1 U3-08-503-799-2	ALIGNMENTS	RESULT 1 US-08-459-493-1 US-08-6105053 Fatent No. 6001638 GENERAL INCORMATION: APPLICANT: Brigham, Kenneth APPLICANT: Condary, John 910 APPLICANT: Canonico, Anglo APPLICANT: PLOSTAGLANDIN SYNTEASE ADDRESSEE: Tilton, Fallon, Lungmus & Chestmut STREET: 100 S. Wacker Drive - Suite 960 CITY: Chicago CITY: US.A. ZIP: 60606-4002 COMPUTER: Illinois COMPUTER: IBM PC Compatible OMPUTER: IBM PC Compatible OMPUTER: DATE PLOYS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/459,493 FILING DATE: 19-AUG-1991 ATTONENY AGAIT INFORMATION: NAME: REPRERENS/DOCKET NUMBER: U99115 REGISTRATION NUMBER: 30 9955 REFERENCS/DOCKET NUMBER: V99115 TELECOMMUNICATION INPERMENTION:	TELEPHONE: (313) 456-8000 ; INPORMATION FOR SEQ ID NO: 1: ; SEQUENCE CERRACTERISTICS: ; LENGTH: 763 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double ; TOPPI/GY: rirollar

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469 GACTITICCIACTIGGCAGIACAICIACIAITIAGICAICGCIAITIACCAIGGIGAIGGGGG 528
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                                                                                                                                        77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                                                                                                                                                                      17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 76
   17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08029022
Setent No. 5641662
GENERAL INFORMATION:
APPLICANT: Debs, Robert J.
APPLICANT: Thu, Ning
TITLE OF INVENTION: TRANSFECTION OF LUNG VIA AEROSOLIZED
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSPRING ADDRESS:
ADDRESSED: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRAIN SAIDS STATE SORM:
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPPRATING SYSTEM: MS-DOS (Version 5.0)
~~FWWARE: WORDPEFECT (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19930310
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,291
FILING DATE: 17 DEC 91
APPLICATION NUMBER: 972,135
FILING DATE: 05 NOV 92
APPLICATION NUMBER: PCT/US92/11008
FILING DATE: 17 DEC 92
ATTORNEY/AGENT INFORMATION:
NAME: RAG-VOLEET, BATDATA
REGISTRATION NUMBER: 32,750
REPERBNCE/DOCKET NUMBER: 05935/008001
TELECOMMUNICATION INFORMATION:
THE DECOMMUNICATION INFORMATION:
THE DECOMMUNICATION INFORMATION:
THE DECOMMUNICATION INFORMATION:
THE DECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/029,022
FILING DATE: 19930310
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TELEPRX: (415) 854-0875
TELEX: 200154
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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: U.S.A.
                                                                                                                                                                                                                                                                                 137 CACCCCA 143
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US-08-029-022-4
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                                                                                                                                                                                                                                                                                                                492 GACTITICOTACITGGGAGTACATCITACTITAGTCATCGCTATTACCATGGTGATGCGG 551
                                                                                                                                                                                                                                           17 GACTITICCTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 76
                                                                                                                                                                                  0; Gaps
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US-08-029-022-2
US-08-029-022-2
IS-08-029-022-2
| Sequence 2, Application US/08029022
| Patent No. 5641662
| GENERAL INFORMATION:
| APPLICANT: Dabs, Robert J.
| APPLICANT: Date | Robert J.
| APPLICANT: Date | Ransgene Delivery |
| TITLE OF INVENTION: TRANSGENE DELIVERY |
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: 4 |
| ADDRESSEE: Fish & Richardson |
| STREET: 2200 Sand Hill Road, Suite 100 |
| CITY: Menlo Park |
| STATE: California |
| COUNTRY: D.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                  Ouery Match 25.4%; Score 127; DB 3; Length 763; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: 13.5" Diskette, 1.44 Mb COMPUTER: 13.5" Diskette, 1.44 Mb COMPUTER: 13.5" Diskette, 15.5X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: 914 DEC 91 FILING DATE: 19930310 CLASSIFTCATION NUMBER: 912,135 FILING DATE: 17 DEC 91 FILING DATE: 17 DEC 92 APPLICATION NUMBER: 972,135 FILING DATE: 17 DEC 92 APPLICATION NUMBER: 972,135 FILING DATE: 17 DEC 92 ATTORNEY AGENT INFORMATION: NAME: RECENTION NUMBER: 92,750 RECENTING DATE: 17 DEC 92 ATTORNEY AGENT INFORMATION: TELECHOMEN: (415) 854-6277 TELECHOMEN: (415) 854-6277 TELECHORS: 015 NO.015 NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 CACCCCA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 CACCCCA 618
LOCATION: 1..763
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US-08-459-493-1
                                                                                                          Query Match
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGGATTTCCAAGTCTC 588
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                                                                                                                                                     Sequence 2, Application US/08246376
Fatent No. 5827703
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STREET: Allfornia
CITY: Menlo Park
STREET: Allfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.4%; Score 127; DB 1; Length 930; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55X
OPERATING SYSTEM: MS-DGS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
PILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 05935/005US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION. 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/92,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/84,498
FILING DATE: June 4, 1992
ATONNEY/ABORT INFORMATION:
NAME: BALBARA RABE-VENTER
REGISTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                    589 CACCCCA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 CACCCCA 143
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137 CACCCCA 143
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US-08-246-376-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                        US-08-246-376-2
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RESULT 5

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469 GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG 528
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US-08-246-376-4

Sequence 4, Application US/08246376

Patent No. 2827703

Patent No. 2827703

APPLICANT: Robert J. Debs

APPLICANT: Ning Zhu
TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: 158h & Richardson
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/894,498
FILING DATE: June 4, 1992
ATTORNEY/AGENT INFORMATION:
RAPISTRANCE/DOCKET NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 37,750
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07972135
Patent No. 5858784
GENERAL INPORMATION:
APPLICANT: Robert J. Debs
TITLE OF INVENTION: GENES IN THE
TITLE OF INVENTION: GENES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:

COMPUTER TIRM PS.2 Model 502 or 558X
OPRATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                                                           CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
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US-07-972-135-2
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ORRESPONDENCE ADDRESS

LUNG BY AEROSOL - AND

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77 ITTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GACTITECTACTIGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
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US-09-256-004-2
i Sequence 2, Application US/08256004
j Patent No. 6001644
j TITLE OF INVENTION:
j TITLE OF INVENTION: IN VIVO TRANSFECTION WITH A CFTR CODING TITLE OF INVENTION: SEQUENCE
j CORRESPONDENCE ADDRESS:
j ADDRESSEE ADDRESSE;
j ADDRESSEE COOLEY GOGWARD CASTRO Huddleson & Tatum STREET: S Palo Alto Square
j CITY: Palo Alto
start: California
cOUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
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25.4%; Score 127; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 COMPUTEK: LDG. C./.
COMPUTEK: SSSX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: MordPerfect (Version SOPTWARE: 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: NO. 5859784ember 5, 1992
CLASSIFTCATION DATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: December 17, 1991
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
APPLICATION NUMBER: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter:
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
RELEVALUMENTION STATEMATION:
TELEPHONE: (415) 854-0875
TELEFAR (415) 854-0875
TELEFAR SOULS4
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARRACTERISTICS:
                       ADDRESSE: Fish & Richardson STREET: 2200 Sand Hill Road, STREET: Suite 100 CITY: Menlo Park STATE: California COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER FORM: 155 Model 502 or COMPUTER: 155 Model 502 or COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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US-07-972-135-4
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100.0%; Pred. No. 2.5e-57;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENES IN THE
LUNG BY AEROSOL - AND
LIPOSOME-BASED
DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: S5SX
COMPUTER: S5SX
COMPUTER: S5SX
SOFTWARE: WordPerfect (Version S.0)
SOFTWARE: S.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: NO. 5858784ember 5, 1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: NO. 5858784ember 5, 1992
FILING DATE: December 17, 1991
APPLICATION NUMBER: 07/809,291
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 32,750
REGISTRATION NUMBER: 32,750
REFINENCE DOCKET NUMBER: 05935/007US1
TELEPHONE: (415) 6854-5277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPRESSION OF CLONED
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or
COMPUTER: 555X
TITLE OF INVENTION: LUNG BY AEROSOL-
TITLE OF INVENTION: LIPOSOME-BASED
TITLE OF INVENTION: LIPOSOME-BASED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 2200 Sand Hill Road,
STREET: Suite 100
CITY Menlo Park
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-972-135-4

Sequence 4, Application US/07972135

Patent No. 585874

Patent No. 586874

APPLICANT: Robert J. Debs

TITLE OF INVENTION: EXPRESSION OF

TITLE OF INVENTION: LING BY ARROSC

TITLE OF INVENTION: LING BY ARROSC

TITLE OF INVENTION: LINGSWE-BASEE

TITLE OF INVENTION: LINGSWE-BASEE

TITLE OF INVENTION: LIPOSOME-BASEE

TITLE OF INVENTION: DELIVERY

NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 CACCCCA 143
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469 GACTITICCIACIIIGGCAGIACAICIACGIAIIIAGICAICGCIAIIAACCAIGGIGAIGCGG 528
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Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09006841
| Patent No. 6468796
| GENERAL INFORMATION: |
| CENERAL INFORMATION: |
| TITLE OF INVENTION: EXPRESSION OF CLONED |
| TITLE OF INVENTION: LING BY ARROSOL - AND TITLE OF INVENTION: LIPOSOME-BASED |
| TITLE OF INVENTION: DELIVERY |
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: | Fish & Richardson |
| STREET: 2200 Sand Hill Road, |
| STREET: Suite 100
           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.50X
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOSPTWARE: WORDERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/07/972,135
FILING DATE: December 17, 1991
ATTORNEY AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05,935/007US1
TELEPHONE: (415) 844-0875
TELEPHONE: (415) 844-0875
TELEPHONE: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENES IN THE
LUNG BY AEROSOL - AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfert (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 CACCCCA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-006-841-2
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US-09-006-841-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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Query Match

25.4%; Score 127; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
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GENES IN THE
LUNG BY ARROSOL - AND
LIPOSOME-BASED
DELIVERY
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Sequence 2, Application US/09006841
Patent No. 6468798
GENERAL INFORMATION:
APPLICANT: Robert J. Debs
TITLE OF INVENTION: EXPRESSION OF TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME-BASEC TITLE OF INVENTION: LINCSOME ADDRESSES:
ADDRESSEE: SAUTE 100 HILL ROAD, STREET: CALIFORNIA RICHARDAN, STREET: CALIFORNIA STREET: CALIFORNIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 CACCCCA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-256-004-2
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529 Triridocagracarcaardddcgraddagcedrirdacrcadddgagarriccaagrcic 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GACTITICCIACTIGGCAGIACATCIACGIATIAGICAICGCIATIACCAIGGIGAIGCGG
                                                                                                                                                                                                                                                                                                                                                                                                 Length 930,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO TITLE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARREST: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.4%; Score 127; DB 5; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0;
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COMPUTER READABLE FORM:
MEDIUM TYRE: 3.5" Diskette, 1.44 Mb
MEDIUM TYRE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM P6/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05366
FILING DATE: 04-UNN-1993
                                                                                                  05935/005US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/92,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 07/927,200
FILING DATE: August 6, 1992
APPLICATION NUMBER: 07/894,498
FILING DATE: June 4, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application PC/TUS9305366
GENERAL INFORMATION:
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REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 0593:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-6875
FILING DATE: June 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: BALDARA RAG-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 0593:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEPHAX: (415) 854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Robert J. Debs
APPLICANT: Ning Zhu
                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                   rYPE: nucleic acid
stranusmuss: single
ropou.ogy:
ropou.ogy:
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STATE: California
COUNTRY: U.S.A.
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PCT-US93-05366-4
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; Sequence 2, Application PC/TUS9305366
; GENERAL INFORMATION:
    APPLICANT: Robert J. Debs
    APPLICANT: Ning Zhu
    TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IN VIVO
    TITLE OF INVENTION: GENE THERAPY
    NUMBER OF SEQUENCES:
    ADDRESSEE: Fish & Richardson
    STREET: 2200 Sand Hill Road, Suite 100
    CITY: Menlo Park
    STATE: California
    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.4%; Score 127; DB 4; Length 930; Best Local Similarity 100.0%; Pred. No. 2.5e-57; Matches 127; Conservative 0; Mismatches 0; Indels
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/972,135
FILING DATE: NO. 6468798ember 5, 1992
APPLICATION NUMBER: 07/809,291
FILING DATE: December 17, 1991
ATTORNEY/AGENT INFORMATION:
NAME: BATDAR RES - Venter
REGISTRATION NUMBER: 32 75
TELEPHONE: (415) 854-5277
TELEPHONE: (415) 854-5277
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APPLICATION NUMBER: PCT/US93/05366
FILING DATE: 04-JUN-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/992,687
FILING DATE: December 17, 1992
APPLICATION NUMBER: 67/927,200
FILING DATE: AUGUST 6, 1992
APPLICATION NUMBER: 07/944,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 555X
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOPTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 854-087
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCCCA 143
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Sequence 7, Application US/08522841

Sequence 7, Application US/08522841

Sequence 7, Application US/08522841

Sequence 7, Application US/08522841

Sequence 7, Application US/0852841

APPLICANT: Belidegrun, Arie 8.

APPLICANT: Belidegrun, Arie 8.

TITLE OF INVENTION: The Prostate Specific Antigen (PSA) Promoter and Uses TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant and Gould

STREET: 11150 Santa Monica Blvd., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 GACTITICCTACTIGGCAGIACAICTACGIATIAGICCAICGCIATIACCAIGGIGAIGCGG 392
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  77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
                                               412 Triridecaciacarcaargesceresarascestrireacircacessarriccaasicre 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 25.4%; Score 127; DB 2; I Best Local Similarity 100.0%; Pred. No. 2.4e-57; Matches 127; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REPERENCE/DOCKET NUMBER: 3043E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                       137 CACCCCA 143
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California
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US-08-522-841-3
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APPLICANT: Wittig, Prof. Burghardt
APPLICANT: Wittig, Prof. Class
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
TITLE OF INVENTION: Therapy
FILE REFERENCE: XI 597/59
CURRENT APPLICATION NUMBER: US/09/310,842A
CURRENT FILING DATE: 1999-05-12
EARLIER FILING DATE: 1996-05-12
EARLIER FILING DATE: 1996-11-13
SOFTWARE: PAPLICATION NUMBER: 206-11-13
SOFTWARE: PAPLICATION NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)._(2)
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to OTHER INFORMATION: 2 can be modified with amino or caroxy features
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OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
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25.4%; Score 127; DB 4; Length 1078;
Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                    Length 930;
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Best Local Similarity 100.0%; Pred. No. 2.5e-57;
Matches 127; Conservative 0; Mismatches 0;
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LOCATION: (1)..(1078)
OTHER INPORMATION: bcr3=abl2; Oligo DNA Dumbbell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09310842A Patent No. 6451593 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 930
                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCCCA 595
                                                                                                                                                      ; TOPOLOGY: linear
PCT-US93-05366-4
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LENGTH: 1078
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US-09-310-842-1
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GENERAL INFORMATION:
APPLICANT: Belidegrum, Arie S.
APPLICANT: Belidegrum, Arie S.
APPLICANT: Belidegrum, Arie S.
APPLICANT: Belidegrum, Arie S.
APPLICANT: Belidegrum, Arie S.
AUGRES GENERAL BELIDEGRUM: No. 591652e1 Nucleic Acid Molecules Comprising
TITLE OF INVENTION: Thereof and Gould
ADDERSIS: Morchant and Gould
CORRESPONDENCE ADDRESS:
ADDRESS: Morchant and Gould
CONNETS: 1130 State Monica Bird., Suite 400
CONNETS: Cliffordes
CONNETS: Belidegrum, Arie S.
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Search completed: February 15, 2004, 19:10:12 Job time : 40.7706 secs

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RESULT 1
US-09-921-143-36
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LENGTH: 52
                                                                                                                                                                                          February 15, 2004, 16:21:35; Search time 210.032 Seconds (without alignments) 8769.219 Million cell updates/sec
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cgn2_6/ptodata_1/pubpna_/USO6_NEW_PUB.seq:*

cgn2_6/ptodata_1/pubpna_/USO6_NEW_PUB.seq:*

cgn2_6/ptodata_1/pubpna_/USO6_PUBCOMB.seq:*

cgn2_6/ptodata_1/pubpna_/DEO6_PUBCOMB.seq:*

cgn2_6/ptodata_1/pubpna_/DEO8_NEW_PUB.seq:*

cgn2_6/ptodata_1/pubpna_/DEO8_NEW_PUB.seq:*

cgn2_6/ptodata_1/pubpna_/USO8_NEW_PUB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2449703 seqs, 1841816367 residues
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	sequence 36, Appl	Seguence 35, Appl	Sequence 1, Appli	Sequence 33, Appl	Sequence 425, App	Sequence 425, App	Sequence 68, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 69, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 33, Appl	Sequence 25, Appl	Sequence 25, Appl
	ID	US-09-921-143-36	US-10-268-927-35	US-09-911-020A-1	US-10-268-927-33	US-09-895-828-425	US-10-114-666-425	US-09-965-703-68	US-10-437-830-3	US-10-465-156-1	US-10-152-363A-69	US-10-206-747-2	US-10-206-747-4	US-09-845-416-33	US-08-900-220C-25	US-09-151-999-25
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	Query Match Length DB	5283	351	412	544	909	600	619	645	851	884	930	930	987	966	966
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Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 6, Appli	7 W T W	Sequence 2, Appli Sequence 2, Appli Sequence 16, Appli Sequence 13, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli
1 US-09-187-387-25 1 US-09-827-110-25 3 US-09-238-243-25 5 US-10-205-534-6	US-10-228-811- US-10-228-811- US-10-228-811- US-10-238-811- US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8 US-09-886-942-8	5 US-10-078-167-2 5 US-10-023-969-4 5 US-10-136-837-2 5 US-10-369-116-3 2 US-10-369-121-43 2 US-10-369-121-43 5 US-10-234-406-3 5 US-10-234-406-3 1 US-09-134-949-1 US-09-392-462-1 US-09-392-462-1 US-09-392-462-1 US-09-392-462-1 US-09-392-462-1 US-09-392-462-1 US-09-392-462-1 US-09-392-462-1 US-10-123-1-3 3 US-10-291-1 3 US-10-291-1
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ALIGNMENTS

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181 ACGAGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240
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| Sequence 36, Application US/09921143
| Publication No. US20030215921A1
| GENERAL INFORMATION:
| APPLICANT: COLDERN, Timothy
| TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
| FILE REPERENCE: PF112P6
| CURRENT APPLICATION NUMBER: US/09/921,143
| CURRENT FILING DATE: 2001-08-03
| PRIOR APPLICATION NUMBER: 60/223,276
| PRIOR FILING DATE: 2000-08-04
| NUMBER OF SEQ ID NOS: 36
| SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                   100.0%; Score 500; DB 13;
llarity 100.0%; Pred. No. 8.8e-272;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: homo sapiens
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Best Local Simi:
Matches 500;
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Gaps

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327 ITTTGGCAGTACATCAATGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 386
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Pred. No. 5.1e-61;
                                                                                                                                                                                                           Query Match 25.4%; Score 127; DB 11; Best Local Similarity 100.0%; Pred. No. 5.1e-61; Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wain-Hobson, Simon
APPLICANT: Blancou, Philippe
APPLICANT: Chenciner, Nicole
TITLE OF INVENTION: HIV RECOMBINANT VACCINE
FILE REPRERENCE: 03495.0239-00000
CURRENT APPLICATION NUMBER: US/10/268,927
CURRENT FILING DATE: 2002-10-11
PRIOR PAPLICATION NUMBER: 06/328,449
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
LENGTH: 544
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25.4%; Score 127; DB
Best Local Similarity 100.0%; Pred. No. 5.1
Matches 127; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/911,020A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 33, Application US/10268927; Publication No. US20030175693A1; GENERAL INFORMATION:
                  2001-07-23
                  CURRENT FILING DATE: 2001-07-
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
                                                                                                                                         ORGANISM: Cytomegalovirus US-09-911-020A-1
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                                                                                       SEC ID NO 1
                                                                                                                           TYPE: DNA
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  181 ACGAGACTITCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGGC 240
                                                                                       241 AACATGCTTATGTAACGGTGAGTTAGCAACATGCCTTATAAGGAGAGAAAAAGCACCGTG 300
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Publication No. US20030040100A1
GENERAL INFORMATION:
APPLICANT: BROUGH, DOUGLAS E
APPLICANT: KOVESII, IMRE
TITLE OF INVENTION: CELL FOR THE PROPAGATION OF ADENOVIRAL VECTORS
FILE REFERENCE: 209459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blancou, Philippe
APPLICANT: Chenciner, Nicole
TITLE REPERENCE: O495.0239-00000
CURRENT APPLICATION NUMBER: US/10/268,927
CURRENT PILICA DATE: 2002-10-11
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: recombinant promoter US-10-268-927-35
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APPLICANT: Wain-Hobson, Simon
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Matches 127; Conservative
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US-09-911-020A-1
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Sequence 425, Application US/09895828
Patent No. US20020099012A1
GENERAL INFORMATION:
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Gaps

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RESULT 8
US-10-437-830-3
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                                                                                                                                                                                                                                                                                                                                                                                                               25.4%; Score 127; DB 9; Length 600; 100.0%; Pred. No. 5.1e-61; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.539C1
CURRENT APPLICATION NUMBER: US/10/114,666
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 479
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                          APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.21.539
CURRENT APPLICATION NUMBER: US/09/895,828
CURRENT APPLICATION NUMBER: 2001-06-28
NUMBER OF SEQ ID NOS: 473
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 425, Application US/10114666 Publication No. US20030103994A1 GENERAL INFORMATION: APPLICANT: Watanabe, Yoshihiro
Nang, Tongtong
McNeill, Patricia D.
Watanabe, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.4
Best Local Similarity 100.
Matches 127; Conservative
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CORGANISM: Homo sapiens
US-10-114-666-425
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-895-828-425
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Matches 127; Conserv
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LENGTH: 600
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US-US-YDS-VUS-US
Sequence 68, Application US/09965703
Sequence 68, Application US/09965703
Patent No. US20020119521A1
GENERAL INFORMATION:
APPLICANT: Rohm and Haas Company
APPLICANT: Palli, Subba Reddy
APPLICANT: Palli, Subba Reddy
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: Cress, Dean Ervin
APPLICANT: APPLICATION NUMBER: 60/19,265,703
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2010-03-22
PRIOR FILING DATE: 2010-03-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENT NOS: 75
LENGTHANE: PATENT NOS: 75
LENGTHANE: PATENT NOS: 75
LENGTHANE: PATENT NOS: 75
LENGTHANE: DATE: 2010-03-21
SEQ ID NO 68
LENGTH: 619
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25.4%; Score 127; DB 13;
Best Local Similarity 100.0%; Pred. No. 5.1e-61;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature; OTHER INFORMATION: No. US20020119521Alel Sequence
US-09-965-703-68
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US-10-437-830-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Cytomegalovirus
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256 GACTITICCIACITIGGCAGIACAICIACGIAITAGICAICGCIATIACCAIGGIGAIGGGG 315
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                                                                                                                               Length 884;
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COMPUTER: IEBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,747
FILING DATE: 11-Feb-2003
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: US 07/809,292
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/894,498
FILING DATE: 04-JUN-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/922/11004
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: WO PCT/US92/11004
FILING DATE: 17-DEC-1993
APPLICATION NUMBER: WO PCT/US93/05366
FILING DATE: 17-DEC-1993
APPLICATION NUMBER: US 08/44,899
FILING DATE: 17-DEC-1993
APPLICATION NUMBER: US 08/44,899
FILING DATE: 04-JUN-1995
FILING DATE: 12-DEC-1992
APPLICATION NUMBER: US 09/132,391
FILING DATE: 12-DAN-1996
ATTORNEY/AGENT INFORMATION:
ANDER: MANCE FEATH DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: US DATE: U
; OTHER INFORMATION; CMV enhancer/MPSV LTR promoter construct.
US-10-152-363A-69
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CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mycroft, Frank J.
REGISTRATION NUMBER: 46,946
REFERENCE,DOCKET NUMBER: 023070-064833US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                        Query Match
25.4%; Score 127; DB 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-61;
Matches 127; Conservative 0; Mismatches 0;
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Publication No. US20030109475A1
GENERAL INFORMATION:
APPLICANT: (1) APPLICANT:Zhu, Ning
(1) APPLICANT:Zhu, Ning
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-10-206-747-2
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| Sequence 1, Application US/10465156 |
| Sequence 1, Application No. US20030232414A1 |
| GENERAL INPORMATION: OUTS. |
| GENERAL INPORMATION: HYBRID VECTOR HAVING A CYTOWEGALCOVIRUS |
| TITLE OF INVENTION: HYBRID VECTOR HAVING A CYTOWEGALCOVIRUS |
| TITLE OF INVENTION: BENHANCER AND MYELOPROLIFERATIVE SARCOMA VIRUS PROMOTER |
| TITLE OF INVENTION: 02-15 |
| CURRENT FILING DATE: 2003-06-18 |
| CURRENT FILING DATE: 2003-06-18 |
| NUMBER OF SEQ ID NOS: 16 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 1 |
| LENGTH: 951
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       GACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
                                           431 GACTITICCTACITIGGCAGIACATCTACGIAITAGTCATGCCIATTACCAIGGIGAIGGGG
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Publication No. US20030103986A1

GENERAL INFORMATION:
APPLICANT: Gross, Wark W.
TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REPERENCE: 01-20
FURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT FILING DATE: 2002-05-20
PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: ASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.4%; Score 127; DB 12; Length 85 Best Local Similarity 100.0%; Pred. No. 5.2e-61; Matches 127; Conservative 0; Mismatches 0; Indels
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TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 33, Application US/09845416

Publication No. US20030171312A1

GENERAL INFORMATION:

APPLICAT: XIAO,

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/845,416

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: 60/200,777

PRIOR APPLICATION OWNER: 306

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 987
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APPLICATION NUMBER: US 09/132,391
FILING DATE: 08-No. US20030109475A1-1998
ATTOREX/AGENT INFORMATION:
NAME: MYCOÍL, FYANK J.
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 023070-064833US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%; Score 127; DB 15;
100.0%; Pred. No. 5.2e-61;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                 TELEX: cUNKNOWN>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 930 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CRGANISM: Homo sapiens
US-09-845-416-33
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Best Local Similarity
Matches 127; Conserval
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IIILE OF INVENTION: Methods and Compositions for In Vivo
Gene Therapy
                                                                                                                                                                                                                                                                                                                                                                                                       Length 930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORREST: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: ADTENTION DATA:
CONTURER: LING PATE:
CONTURER: IL FEB-2003
CLASSIFICATION NUMBER: US/10/206,747
FILING DATE: 11-Feb-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
CLASSIFICATION DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/992,687
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: WO PCT/US92/11004
FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-DEC-1992
APPLICATION NUMBER: WO PCT/US93/05366
FILING DATE: 04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/809,292
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/84,498
FILING DATE: 04-UN-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 06-MG-1992
APPLICATION NUMBER: US 07/927,200
FILING DATE: 05-NOV-1992
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FILING DATE: 22-JAN-1996
                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: (i) APPLICANT: Zhu, Ning (i) APPLICANT: Zhu, Ning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10206747 Publication No. US20030109475A1 GENERAL INFORMATION:
              (415) 576-0300
                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 930 base paire
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 25, Application US/09151999
; Patent No. US20020151460A1
; GENERAL INFORMATION:
APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                                                                                                                                                                                                                              TITLE OF INVENTION: Method of Treating Dopaminergic and GABA-nergic Disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.4%; Score 127; DB 8; Length 996; Best Local Similarity 100.0%; Pred. No. 5.2e-61; Matches 127; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: ONV-044.01
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: AscII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,220C
FILING DATE: 24-Jul-1997
CLASSIFICATION: <URKINOM:>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTA: ....
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
RADRESSER: FOLBY, HOAG & ELIOT LLP
STREET: ONE POST OFFICE SQUARE
CITY: BOSCON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-900-220C-25
                                                                                                                    APPLICANT: Miao, Ningning
Wang, Monica
Mahanthappa, Nagesh K.
                                              Sequence 25, Application US/08900220C Publication No. US20020045206Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 25:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                      Pang, Kevin
Jin, Ping
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 32
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RESULT 14
US-08-900-220C-25
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77 TITIGGCAGTACATCAATGGGGCTGGATAGGGGTTTGACTCACGGGGATTTCCAAGTCTC 136
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                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Description of Artificial Sequence: gene, OTHER INFORMATION: activation construct US-09-151-999-25
FILE REFERENCE: ONV-031.02
CURRENT APPLICATION NUMBER: US/09/151,999
CURRENT FILING DATE: 1998-08-11
EARLIER APPLICATION NUMBER: 08/955,552
RARLIER FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 28
SEQ ID NOS: 28
SEQ ID NO 25
LENGTH: 996
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Job time : 213.032 secs
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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B1489763 603032280
B1489620 603032080
B1490268 603032080
B1490463 603032280
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1 aagcttgaccttatgcgact.....cacctgggttgggatcgatc 500
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                          OM nucleic - nucleic search, using sw model
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12 BI489620
12 BI490268
12 BI490463
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/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anorymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1:3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
/note="Organ: pooled brain, lung, testis; Vector:
pcw-SPORT6; Site 1: Not1; Site 2: ECORV (destroyed); RNA
source annonymous pool of e male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: Gapbarr@mail.nih.gov

rissue Procurrement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Phate: LLAM1131 row: o column: 20
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B"
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//lab_host="DHIOR"
//lone_lib="WIH MGC_IIS"
//note="Corgan: polol@ brain, lung, testis; Vector:
//note="Corgan: polol@ brain, lung, testis; Vector:
//note="Corgan: polol@ brain, lung, testis; Vector:
//note="Corgan: polo@ brain, lung, testis; Vector:
//note="Corgan: polog@ brain, lung, langer range 23-27; lungle lung, age 27; and 1 male brains, age 69. Library is
//notec along and directionally cloned (EcoRV site is
//notect primed and directionally cloned (EcoRV site is
//notect polog -13 kb. Library is normalized and
//notect pologen: Research Genetics tracking code
//notect pologen: Research Genetics tracking code
//notect pologen: NIH MGC Library."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov
Plate: LLAMIA131 row: o column: 20

High quality sequence stop: 191.
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                                                                                  /mol_type="mRNA"
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/clone="IMAGE:5173506"
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BZ996651 480 bp DNA linear GSS 25-MAR-2003 PUBKH77TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa074N10, genomic survey sequence.
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1 (bases 1 to 480)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Unpublished
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/note=rected genomic DNA library"
                                          17 GACTITCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
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25.4%; Score 127; DB 29; Length 480;
Best Local Similarity 100.0%; Pred. No. 6.5e-58;
Matches 127; Conservative 0; Mismatches 0; Indels 0
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/strain="B73"
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BZ996651.1 GI:29240068
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//dlob_libe=wilth MCC_115"
//dlob=libe=wilth MCC_115"
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Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 193)

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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LIAL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiAL at:
http://image.llnl.gov. p column: 19
Plate: LLAMI1431 row: p column: 19
High quality sequence etcp: 193.
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NIN-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH MGC Library." 50 c 46 g 38 t
                                                                                                                                                                 Score 127; DB 12; Length 193;
Pred. No. 5.6e-58;
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25.4%; Score 127; DB 12; Length 193;
Best Local Similarity 100.0%; Pred. No. 5.6e-58;
Matches 127; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                      Query Match
25.4%; Score 127; DB
Best Local Similarity 100.0%; Pred. No. 5.6e
Matches 127; Conservative 0; Mismatches
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                                                                      46 g
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GSS 05-FEB-2003
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AV645385

AV645385 GLA Homo sapiens cDNA clone GLAAAG02 3', mRNA sequence.
AV645385

AV645385.1 GI:9866399
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/clone_lib="CIT978SK"
/note="Vector: pBAC108L; Site_l: HindIII; Site_2: HindIII;
Clote="Weftor: Davary A"
- 159 c 165 g 140 t
Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
1741: 301 838 0200
Fax: 301 838 0208
Faxi: 301 838 0208
Gmail: madams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
1el: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.8h.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"

mol_type="genomic DNA"

db_xref="gdb:726476"

/db_xref="taxon:9606"

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1 (Dases 1 to 610)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H., Simon, M. and Venter, J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B68191 CIT978SK-A-492C12.TV CIT978SK Homo sapiens genomic clone A-492C12,
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/organism="Zea mays"

/organism="Zea mays"

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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick
Whitelaw, C.A., Vackenbush, J., Van Aken, S., Utterback, T., Resnick
A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
Maize Genomics Consortium
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                               PUBIS38TD ZM_0.6_1.0 KB Zea mays genomic clone ZMMBTa064H03,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA
Par: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.4%; Score 127; DB 29; Length 5
100.0%; Pred. No. 6.5e-58;
tive 0; Mismatches 0; Indels
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Other_GSSs: CIT978SK-A-492C12.TP
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                                                                                                                                            BZ680401.1 GI:28235262
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Best Local Similarity 100.
Matches 127; Conservative
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AV645392 AAN-2002 AVAN-2002 AVAN-2002 AV645392 GLA Homo sapiens cDNA clone GLAAAG09 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarthin; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarthin; Hominidae; Homo.

Mu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,

Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,

Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,

Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level

by comparing gene expression profiles of hepatocellular carcinoma

with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2011)
                                                                                                                                                                                                                                   384 GACTITICCTACTIGGCAGIACAICIACGIAITAGICAICGCIAITACCAIGGIGAIGCGG 325
                                                                                                                                                                                                                                                                          77 TITITGGCAGTACATCAAIGGGCGIGGATAGCGGITITGACTCACGGGGAITITCCAAGICIC 136
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note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Ji Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801912
Email: hanzgeoto.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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dev stage="Adult"
lab_host="SOLR"
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Pred. No. 6.8e-58;
                                                                                                            Score 127; DB 9;
Pred. No. 6.8e-58;
                                                                                                25.4%; bcc. No. c. 100.0%; Pred. No. c. 0; Mismatches
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100.0%; Pred. No. v..
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/db_xref="taxon:9606"
/clone="GLAAAG09"
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1 (Dases I to 634)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, O., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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|note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                             ('tissue type="corresponding non cancerous liver tissue"
dev stage="Adult"
lab_host="SOLR"
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 619
/organism="Homo sapiens"
/mol_type="MRNA"
/db_xref="texon:9606"
/clone="GLABARG02"
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Lone is available at CHGC in Shanghai.
Location/Qualifiers
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Pred. No. 6.8e-58;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLAAAG07"
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lab_host="SOLR"
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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385 GACTITCCTACTIGGCAGIACATCTACGIATIAGICAICGCTATIACCAIGGGGG 326
                                                            325 Trirgacagracarcaardagacardaaradagarrirgacicacagagarrirccaagicrc 266
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 640)
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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                              TITIGGCAGIACATCCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTC
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
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100.0%; Pred. No. 6.8e-58;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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AV645393/c
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AV681492 GXA Homo sapiens cDNA clone GKAAAD01 5', mRNA sequence.
AV681492 AX HOMO SAPISS SARAAD01 5', mRNA sequence.
AV681492.1 GI:10283355
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I bases I to 64.

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, X., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15094 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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AV681509 GKA Homo sapiens cDNA clone GKAAAC02 5', mRNA sequence.
AV681509
               Email: thomas_look@dfci.harvard.edu
The clone was Obtained from an RZPD array made from an adult kidney
CDNA random primed library from Leonard Zon. RZPD library number
576. This clone is available from the Resource Centre/Primary
Database of the German Human Genome Project: RZPD (Ressourcen
Sentrum Primr Datenbank). http://www.rzpd.de
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-508019192
Fax: 86-21-508019192
Fax: 86-21-5080191972
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                /organism="Danio rerio"
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library no: 576"
/note="Organ: Kidney; Vector: pBK-CMV"
/note="Organ: Kidney; Vector: pBK-CMV"
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llarity 100.0%; Pred. No. 6.8e-58;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Tel: (617) 632-5826
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               Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
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                                                                                                                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
S15 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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100.0%; Pred. No. 6.8e-58;
tive 0; Mismatches 0;
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Dana-Farber Cancer Institute
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ncleic - nucleic search, using sw model	on: February 15, 2004, 19:10:26; Search time 3961.99 Seconds (without alignments) 10335.846 Million cell updates/sec	e: US-09-921-143-36_COPY_2000_3000 ect score: 1001 l tctcaggctaaccagtggggttcggctgcggcgagcggta 1001 ing table: OLIGO_NUC Gapop_60.0 , Gapext 60.0	thed: 2	size : 0 1 number of hits satisfying chosen parameters: 5777422	mum DB seq length: 0 mum DB seq length: 200000000	-processing: Listing first 45 summaries	GenEmbl:* 2: qb ba:* 2: qb ba:* 4: qb ba:* 5: qb on:* 6: qb pat:* 7: qb pat:*
	Run on:	Title: Perfect score Sequence: Scoring table		Jer		Post-processing	Database :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

COTE MATCH LENGTH DB ID MACHINGS 2 AC0996563 679 67.8 278936 2 AC099665 494 49.4 1146 10 RNINS2 358 35.8 3990 6 A30509 343 34.3 2852 10 RATINSII 290 29.0 584 6 AX35792 290 29.0 584 6 AX35792 290 29.0 584 6 AX357379 290 29.0 584 6 AX357379 290 29.0 713 6 AR15489 290 29.0 713 6 AR15489 290 29.0 713 6 AR15489 290 29.0 714 6 AR15489 290 29.0 715 6 BD182736 290 29.0 716 6 AR15489 290 29.0 717 6 AR15489 290 29.0 718 6 AR151919 290 29.0 718 6 AR15489 290 29.0 718 6 AR151919 290 29.0 718 6 AR151919 290 29.0 718 6 AR151919 290 29.0 770 6 BD124786 290 29.0 770 6 BD124786 290 29.0 770 6 BD124786 290 29.0 778 6 AR151919 290 29.0 778 6 AR15194 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR15195 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR15195 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR151919 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154650 290 29.0 778 6 AR154662 290 29.0 778 6 AR154662 290 29.0 778 6 AR154670 290 29.0 778 6 AR15787 290 29.0 778 6 AR	Description	AC098563 Rattus no AC099449 Rattus no	243	A30511 Plasmid p26	v 4	43 Ricin-1	E33315 Compound al	AR276491 Sequence	AX063012 Sequence	AX351379 Sequence	AR072501 Sequence	AR274302 Sequence AR072503 Sequence	AR274304 Sequence	A85396 Sequence 55 AR154889 Sequence	E65414 Genome DNA	AR072502 Sequence	AF261959 Anourosor	AR036905 Sequence AD141144 Sequence	AR181919 Sequence	AF261960 Anourosor AX197652 Semience	AJ489202 Beta nana	AF261962 Anourosor RD124786 Drimer fo	BD126222 Primer fo	AF261963 Anourosor	AA263/44 Sequence AR244231 Sequence	AJ489201 Beta nana	AR244167 Sequence AJ244003 Lepilemur	AX046223 Sequence	AR244042 Sequence	1416	2989 Sequence	AKU/8234 Sequence AR154630 Sequence		DNA linear HTG 13-MAY-2003 5. WORKING DRAFT SECUENCE.	FULLTOP.	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;	Abramzon,S., Adams,C., Alder,J., , Amin,A., Anguiano,D.,
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Anyelbechni, N. Aoyagi, A. Ayodeli, M., Barnated, M., Bandamed, F., Bildarin, D., Bandaranike, D., Barber, M., Barnated, M., Bendamed, F., Bishardo, K., Burch, P., Barce, M., Bendamed, F., Bishardo, K., Burch, P., Barce, M., Brando, K., Bulta, V., Balar, W., Barnebhurg, K., Bithar, M., Calderon, E., Cardens, V., Carter, K., Calderon, E., Cardens, V., Carter, K., Calderon, E., Cardens, V., Carter, K., Canderon, E., Carter, M., Cocker, M., Cocker, M., Carter, M., Calderon, E., Dania, M., Davis, C., Cocker, M., Carter, M., Cocker, M., Day, K., Drando, C., Ding, M., Chen, E., Dania, D., Dania, C., Day, R., Day, Carter, M., Day, K., Day, K., Day, K., Day, K., Carter, M., Garter, M., Carter, M., Garter, M., Carter, M., Garter, M., Carter, M., Garter, M., Carter, M., Carter, M., Garter, M., Garter, M., Carter, M., Garter, M., Carter, M., Garter, M., Garter, M., Garter, M., Garter, M., Carter, M., Garter, M., Garter, M., Garter, M., Carter, M., Garter, M., Garter, M., Carter, M., Garter, M., Carter, M., Carter, M., Garter, M., Carter, M., Carter, M., Mandar, M., Martin, M., Mallyk, S., Khan, Z., Kiny, J., Kovar, J., Kovar, M., Martin, M., Mallyk, M., Martin, M., Mallyk, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M., Martin, M
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Submitted (13-My-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23664519.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.dgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-casffold'). Within each contig-casffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs-casffold in the clone and there may be sequence contigs each fold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contygs will be indicated in the feature
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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                                                                           Contact: base-helpocm.twn.edu

Contact: project Information
Center project name: GTN
Center project name: GTN
Center clone name: GTN
Center clone name: GTN
Center clone name: GTN
Center clone name: GTN
Assembly program: Atlas 3.0;
Consensus quality: 257140 bases at least Q40
Consensus quality: 257743 bases at least Q20
Consensus quality: 280800 bases at least Q20
Estimated insert size: 269272; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AACAGGATGTGTAGGTTTTTGGAGGCCCATATGTCCATTCATGACCAGTGACTTGTCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
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/note="wgg_contig"
1 64123 c 64880 g 63888 t 20450 others
                                      Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Center: Baylor College of Medicine
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clone_end:Sp6
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                                                                                                                                     47714
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Rattus norvegicus clone CH230-57B2, WORKING DRAFT SEQUENCE, 6
unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                              47715 GIGCIGCIGAIGCICIGCCCIGIGCIGACAIGACCICCCIGGCAGIGGCACAACIGGAGC
                                                                                                                                                                                                       361 GTGCTGCTGATGCTCTGCCCTGTGCTGACATGACCTCCCTGGCAGTGGCACACACTGGAGC
                                                                                                                                                                                                                                                                                                                                                TGGTTGGAGGCCCGGGGGGGGGGGGGCCTTCAGACCTTGGCCACTGGAGGTGGCCCGGCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 ACTGCAACTAGGCCCACCACTACCCTGTCCACCCCTCTGCAATGAATAAAACCTTTGAAA
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HTG; HTGS PHASE1; HTGS DRAFT; F
Rattus norvegicus (Norway rat)
Rattus norvegicus
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ALL SUBMITTERED COMMITTERS SHOULD SUBMITTERED CONTROL SUBMITTERED CONTROL SUBMITTERED CONTROL COLLEGE OF MEDICINE, ONE BAYLOR PLAZA, HOUSTON, TX 77030, USA.

ON MAY 10, 2003 this sequence version replaced gi:23664548.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.chm.lmc.edu/projects/rat/). Each contrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgaan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nari, I., Mankervis, C., Naal, D., Newton, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnunssagoon, A., Palls, S., Parks, K., Pasternak, S., Parks, K., Parat, H., Perca, L., Peranhkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul. -L., Puazo, M., Nen, Y., Rechin, E., Pull, L.-L., Parachin, E., Reeves, K., Regier, M.A., Reigh, R., Raizo, J., Revery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shety, J., Shvartsbeyr, A., Sisson, I., Sitter, C.D., Smajs, D., Shety, J., Shvartsbeyr, A., Stose, M., Tabor, P., Taylor, C., Steinje, R., Sutton, A., Svatek, A., Tarjos, Z., Usman, K., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K., Waight, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K., Wright, R., Waillson, R., Waldron, L., Walker, B., Wang, J., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Von Niederhausern, A., Weise, R., Smith, D., Neinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (115-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

1 (bases 1 to 28862)
Rat Genome Sequencing Consortium.

Direct Submission
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Direct Submission
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1 (bases 1 to 1146)
Lomedico, P., Rosenthal, N., Efstratidadis, A., Gilbert, W.,
Kolodher, R. and Tizard, W.
The structure and evolution of the two nonallelic rat preproinsulin
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/codon_start=1
/poduct="preproinsulin"
/protein_id="CpA24560.1"
/db_xref="G1:56490"
/db_xref="Syss-prot.p01323"
/translation="MALWIRFLPLIALLILWEPRPAQAFVKQHLCGSHLVEALYLVCG
ERGFFYTPMSRREVEDPQVAQLELGGGPGAGDLQTLALEVARQKRGIVDQCCTSICSL
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       601 GAGCACTACAAGTTGTGTGTACATGCGTGCATGTGCATATGTGGTGCGGGGGAACATGA 660
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insulin; preproinsulin.
Kattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 6.4e-278;
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/db xref="taxon:10116"
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498284
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/number=3
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100.0%; Pred. No. c,
... 0; Mismatches
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/note="wgs_contig"
complement(280810. .281
/note="clone_boundary
clone_end.sp6
site:EcoR1
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Best Local Similarity 100.
Matches 679; Conservative
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	A30509 3980 bp DNA linear PAT 0 Plasmid p264BGL. NA30509 A30509.1 GI:23957136 S synthetic construct ISM synthetic construct ISM synthetic construct ISM synthetic construct S synthetic construct ISM synthetic Construct ISM synthetic Construct S synthetic Construct ISM s	methods for their 1 others ; iength 3980;	171 GAGGATGGTAACAGATGTGTAGGTTTTGGAGGCCCATATGTCATTCAT	Oy 291 AGAAAGCCTGGGCTAATCAGGGGTCGCTCCTCTAACTGGATTGTCCTATGGT 350
	OY 481 AGGGGGGCATCGTGGATCAGTGCTGCACCACCTCTCTACCAACTGGAGAACT 540	A30511 3979 bp DNA linear PAT 0 Plasmid p264BAM. NA30511 A30511. A30511.1 G1:23957137 S synthetic construct ISM synthetic construct axinthetic construct CE 1 (bases 1 to 3979) CE 7 (bases 1 to 3979) CR Fountculakis, M., Garotta, G. and Stueber, D.	JOURNAL Patent: EP 0393502-A 78 24-0CT-1990; JOURNAL Patent: EP 0393502-A 78 24-0CT-1990; FRATURES Location/Qualifiers Source 1. 3979 /organism="synthetic construct" /mol type="genomic DNA" BASE COUNT 946 a 988 c 1115 g 930 t	Ouery Match Best Local Similarity 99.6%; Pred. No. 5e-198; Matches 458; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 171 GAGGGATGGTAACAGGATGGTAGGTTTTGGAGGCCATATGTCCATTCATGACCAGTGA 230

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/note="insulin II signal peptide"
1187. .1276
/product="insulin II B-chain"
1881. .1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.3%; Score 343; DB 10;
ilarity 99.4%; Pred. No. 3.3e-189;
Conservative 0; Mismatches 3;
                                                                                                                 982 .1100
/note="ins-II mRNA intron A"
join(1115. .1301,1801. .1946)
/note="preproinsulin II"
                                                                                                                                                                                                                                                                                                                                                                                                                  1881. .1943
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                   organism="Rattus norvegicus"
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'note="ins-II cds intron
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                                       /mol_type="genomic DNA"
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The rat genome contains two nonallelic genes which are similarly expressed and produce very similar end products for preproinsulin. They differ from each other by two AAs in the B-chain and by two AAs in the C-peptide. The coding region of the rat insulin II sequence contains two intervening sequences, the first of which is also found in rat insulin I. The homology extends to about 500 nucleotides upstream of the cap sites, but diverge extensively immediately downstream of their poly-A sites.

In a personal communication, S.Chan [4] noted that the 5' end of the sequence in fig. 5 of [2] is incorrect; hence we have only included the bases 3' to this area.

A TATA box is located at positions 909-914, and a poly-A signal at 1980-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 897 to 2042) including the condition of the condition. Rosenthal, N., Efstratidadis, A., Gilbert, W., Kolodner, R. and lizard, R. The structure and evolution of the two nonallelic rat preproinsulin
                                                                                                                                                                                                                                                                                                                                                        ROD 27-APR-1993
                                                                                                                                                  CAACTGGAGCTGGGTGGAGGCCCGGGGGAGGTGACCTTCAGACCTTGGCACTGGAGGTG 1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
Rattus norvegicus (Abrata)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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So (bases 1 to 2952)

Soares, M.B., Schon, E., Henderson, A., Karathanasis, S.K., Cate, R., Zeitlin, S., Chirgwin, J. and Efstratiadis, A.

ENA-mediated gene duplication: the rat preproinsulin I gene is a functional retroposon

Mol. Cell. Biol. 5 (8), 2090-2103 (1985)
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                                          GCCCGGCAGAAGCGCGCCATCGTGGATCAGTGCTGCACCAGCATCTGCTCTCTTACCAA
                                                                                                                          Chan, S.J., Noyes, B.E., Agarwal, K.L. and Steiner, D.F. Construction and selection of recombinant plasmids containing full-length complementary DNAs corresponding to rat insulins I
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Nat insulin II gene (ins-2) with two introns.
J00748.1 GI:204958
insulin.
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Unpublished (1984)
4 (bases 1103 to 1228)
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Location/Qualifiers

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1 (Dases 1 to 584)
Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S., Carter,D., Retter,M.W., Mannion,J. and Fan,L.
Compositions and methods for the therapy and diagnosis of lung
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/organism='pUC 18'.
Location/Qualifiers
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AR272910
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|/organism="unidentified"
|/mol_type="genomic DNA"
|/db_xref="taxon:32644"
|/db_xref="taxon:32644"
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                                   Ricin-like toxin variants for treatment of cancer, viral or parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                  C12N15/29,C12N15/62,C12N15/70,C12N15/86,A61K38/16,A61K48/00 CC Ricin-like toxin variants for treatment of cancer, viral or CC parasitic
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/organism≈'Baculovirus transfer vector pVL

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"I (bases 1 to 9632)

Borgford, T.

Ricin-like toxin variants for treatment of cancer, viral or parastic infections

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S Baculovirus transfer vector pVL 1393

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                                                                                                                                                                                                                                                                                                                                                30-APR-1998 JP 1998546437
30-APR-1997 US 60/045148,29-OCT-1997 US
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
t 2122 c 2176 g 2733
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JP 2001523961-A/1.
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E33315.1 GI:18624059
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PF 30-APR-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                               Homo sapiens (human)
Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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larity 100.0%; Pred. No. 4.6e-158;
Conservative 0; Mismatches 0; Indels
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CORIXA CORPORATION (US)
Location/Qualifiers
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WO0204514.
                                  AX063012
Sequence 639 from Patent W00100828.
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Sequence 639 from Patent
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1 (bases 1 to 584)
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2 (bases 1, Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.
Compositions and methods for the therapy and diagnosis of lung
                                                                                                      37 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAATTCCACACA
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Best Local Similarity 100.0%; Pred. No. 4.6e-158;
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Sequence 639 from patent US 6509448.
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1 (bases 1 to 701)
Chatterjee,D.K.
Cloned DNA polymerases from thermotoga maritima and mutants thereof Patent: US 5948614-A 24 07-SEP-1999;
Location/Qualifiers
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Hughes, A.J. and Chatterjee, D.K.
Cloned DNA, polymerases from Thermotoga and mutants thereof
Patent: US 6506560-A 24 14-7AN-2003;
Patent: Location/Qualifiers
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Matches 290; Conservative 0; Mismatches 0;
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Sequence 24 from patent US 6506560.
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Sequence 24 from patent US 5948614.
AR072501. GI:9999265
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 100.0%; Score 290; DB 6; Length 65
Local Similarity 100.0%; Pred. No. 4.6e-158;
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Sequence 126 from Patent WO0196390.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
          /mol_type="genomic DNA"
/db_xref="taxon:9606"
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832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 891
                                                                                                       167 CATTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTGGTGGCGAGCTGC 226
Best Local Similarity 100.0%; Pred. No. 4.6e-158; Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: February 16, 2004, 01:25:51 Job time : 3967.99 secs

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8338.264 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Length	DB	Н	Description
1 -	1001	100.0	!	24	ABK10062	Expression vect
ı N	309	30.9	3979		AAQ06312	Sequence of pla
ım	307	30.7		21	AAA58309	pDIP/PyCSP.1 p
4	291	29.1		18	AAT97898	Baculovirus tra
יעו	291	29.1	9632		AAX04251	Baculovirus tra
vo	290	29.0			ABV45293	Human prostate
7	290	29.0		21	AAA10990	Fragment #2 of
· c	000	000			2000BBBB	N. meningitidis

(HUMA-) HUMAN GENOME SCI INC. 04-AUG-2000; 2000US-223276P.

tor asmi lasm ansf exp exp puc s pa

Coleman TA;

Human prostate exp Human lung tumour	encod	Human lung neuroen	ancer thera	ğ	es sedn	colon ca	nervous	nervous	Human reproductive	Human reproductive	DNA encoding novel	Human immune/haema	ocoding huma	Human testicular a	L.	5.	ed prote	secreted	uman secreted pr	N. meningitidis pa	. neapolitana Tn	. meningitidis p	N. meningitidis pa	Plasmid pGEM DNA #	Human immune/haema	uman ove	E. coli J96 pathog	ö	Human cDNA clone r	e muscula	prostate	Human prostate can	T7 promoter sequen	Human prostate can	DNA encoding novel	
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ALIGNMENTS

ABK10062

Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1; chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a; allergic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferative disorder; viral infection; bacterial infection; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; gene therapy. Expression vector construct pVGI.1 containing VEGF-2 insert. ABK10062 standard; DNA; 5283 BP 03-AUG-2001; 2001WO-US24658. (first entry) WO200211769-A1. 21-MAY-2002 14-FEB-2002 Synthetic. ABK10062;

Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischaemia or myocardial ischaemia, autoimmune disorders and allergic conditions

Disclosure, Fig 31; 241pp, English.

The invention relates to an isolated nucleic acid comprising pVGI.1 expression vector construct containing the vascular endothelial growth factor 2 (VEGP-2) insert. The nucleic acid is useful for producing a host cell by transducing, transforming or transfecting a host cell by transducing, transforming or transfecting a host cell with the MDM, and for treating a pattent having chronic limb ischaemia or myocardial ischaemia, or a disease or disorder selected from autoimmune disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g. cond:), hyperproliferative disorders (e.g. Gaucher's disease), diseases due to viral, bacterial, fungal or parasitic infection, diseases us alsorders (e.g. cardiomyopathy), arthythmia, heart valve diseases, aneurysms, arterial occlusive disorders and embolism. This

Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 other;

0; Gaps 100.0%; Score 1001; DB 24; Length 5283; tlarity 100.0%; Pred. No. 6.8e-300; Conservative 0; Mismatches 0; Indels 0; Local Similarity Best Local Sim: Matches 1001; Query Match

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2180 AACAGGAIGIGIAGGIITITGGAGGCCCATAIGICCATICAIGACCAGIGACTIGICTCAC 2239 AGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTG 300 × 241

421

2479 540 2420 resericadescocescos de contra d AGCGCGCCATCGTGGATCAGTGCTGCACCAGCATCTGCTCTCTTTACCAACTGGAGAACT 481

GAGCACTACAAGTTGTGTACATGCGTGCATGTGCATATGTGGTGCGGGGGAACATGA 660

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8660 eredederederedadregreeredegerraarcraacaecaecrereradaceraarear 2719 2720 GGICATAGCIGITICCTGTGTGAAATTGTTATCCGCTCACAATTCCACACACATACGAG 2779 2840 cerrececretececerriceaerecesaaacerereceneeereceaeerecaeerecaeere 2900 TCGGCCAACGCCGGGGAGAGAGCGGTFTGCGTATTGGGCGCTCTTCCGCTTCTCCGCTTA 2959 900 901 TCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCA 960 661 GTGGGGCTGGCTGGAGTGGTCGCGGCTTAATCTATCTGGCAGCTGTCTAGACGTAATCAŢ 841 CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAA 961 CTGACTCGCTGCGCTCGTTCGCTGCGGCGAGCGGTA 1001 2960 craacrecordecresores 3000 721 g d 셤 ठ d 8 원 ò à ઠે

AAQ06312

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AAQ06312 standard; DNA; 3979 BP

AAQ06312;

(updated)
(first entry) 25-MAR-2003 29-JAN-1991 Sequence of plasmid p264BGL

IFN-gamma receptor; autoimmune disease; multiple sclerosis; nypersensitivity; ds.

Homo sapiens,

Location/Qualifiers /*tag= c /label= S.P.1 1288..1292 /*tag= d 243..426 /*tag= b 243..405 279..242 *tag= polyA_signal Sig-peptide Key

EP393502-A.

24-OCT-1990

90EP-0106992 11-APR-1990;

90EP-0106992

11-APR-1990;

(HOFF) HOFFMANN-LA ROCHE AG.

Stuber D; Fountoulakis M, Garotta G, WPI; 1990-322042/43.

P-PSDB; AAR07066

Soluble interferon-gamma receptors - for treating auto-immune diseases, chronic inflammations, etc.

Disclosure, Fig 55; 174pp; English.

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1024 GCTCCTCCTAACTGGATTGTCCTATGTGTTTGCTTCTGTGCTGCTGATGCTCTCCCCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                         1084 GTGCTGACATGACCTCCCTGGCAGTGGCACAACTGGAGCTGGAGGCCCGGGGGCAGC
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                                                                                                                                                                                                                                                                                                                                                     502 GCTGCACCAGCATCTGCTCTCTACCAACTGGAACTACTGGAACTAGGCCCACCACT
                                                                                                                                                           Gabs
IFN-gamma is a therapeutically active agent in the treatment of autoimmune disease, allograft transplant rejections, wultiple sclerosis, chronic inflammations and delayed hypersensitivity. It is also useful in identifying IFN-gamma agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pDIP/PyCSP.1 plasmid; malaria vaccine; circumsporozoite protein;
protozoacide; immunoenhancer; human; rat; ds.
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                                                                                                                         Query Match
30.9%; Score 309; DB 11; Length 3979;
Best Local Similarity 100.0%; Pred. No. 8e-87;
Matches 309; Conservative 0; Mismatches 0; Indels 0;
                                                                                                Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "IL-2 PyCSP fusion protein"
                                                                      (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pDIP/PyCSP.1 plasmid nucleotide sequence.
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/note= "CMV-IE promoter"
933..2369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1324 CATGCGTGC 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  622 CATGCGTGC 630
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                                                        See also AAQ06301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410
                                                                                                                                                                                                                                                                                 The present sequence is the plasmid vector pDIP/PyCSP.1. The vector comprises a gene encoding Plasmodium yoelli dircumsporosoite protein (PyCSP), operably linked to prometer from Cytomegalovirus (CMV.IE). The expression of the CSP gene results in the production of an immune response to the malaria protein and a reduction in malaria parasites at the pre-erythrocytic, erythrocytic, and gametocyte stages of infection. The present sequence can therefore be used as a malaria vaccine. The present sequence has human and rat components also: partial human IL-2 sequence and partial rat preproinsulin II sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 AGAAAGCCTGGGCTAATCAGGGGGTCGCTCAGCTCCTAACTGGATTGTCCTATGTGT 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                Inducing protective immune responses against Plasmodium parasite proteins for controlling malaria in mammals comprises injecting a polymucleotide delivery vector having a DNA sequence coding for the Plasmodium protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ricin; toxin; antiviral; virucide; retrovirus; protease; HTLV-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.7%; Score 307; DB 21; Length 5552; Best Local Similarity 99.3%; Pred. No. 2.9e-86; Matches 457; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5552 BP; 1605 A; 1303 C; 1321 G; 1323 T; 0 other;
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                                                                                                                                                                                                                                               Example 1; Columns 15-22; 21pp; English.
                        Hedstrom RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baculovirus transfer vector pVL1393.
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                      Sedegah M, Hoffman SL,
                                                                WPI; 2000-410681/35
                                                                                      P-PSDB; AAB07288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4482 CATTAATGAATCGGCCAACGCGGGGGGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT 4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4302 ACGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACAC 4361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 ACGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAC 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the DNA sequence of baculovirus transfer vector pVL1393.
A claimed baculovirus transfer vector incorporates a nucleic acid (see AAT97899-901, AAT97910, AAT97915 and AAT97919) that encodes a recombinant protein in which the A and B chains of a ricin-like toxin are linked by a heterologus linker peptide (see AAM96880-86) that contains a cleavage recognition site for a retroviral protease such as HIV, HTLV-1 or HTLV-1. The vector provides expression of the recombinant proteins in Sf9 insect cells. The recombinant proteins can be used to selectively inhibit or destroy mammalian cells infected with a retrovirus, such as cancer cells associated with HIV or cells associated with HIV. The recombinant proteins are non-toxic until the ricin A chain is liberated from the B chain by the retroviral protease, and thus can be used to specifically target infected cells without the need for a cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    831 ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           891 CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT 950
                                                                                                                                                                                                                                                                                                                                         DNAs encoding ricin like toxins A and B - are linked via linker containing cleavage site for retroviral protesse, used to inhibit or destroy mammalian cells infected with retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
cancer, infection, therapy, vector, pVL1393; ds, circular, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%; Score 291; DB 18; Length 9632;
100.0%; Pred. No. 2e-81;
Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9632 BP; 2602 A; 2122 C; 2176 G; 2732 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13, Fig 11, 105pp, English.
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                                                                                                                                                                                        96US-0016509.
                                                                                                                                                  97WO-CA00288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 291; Conservative
                                                                                                                                                                                                                            (CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                         WPI; 1997-549735/50.
                                                                                                                                                  29-APR-1997;
                                                                         WO9741233-A1
                                                                                                                                                                                        30-APR-1996;
                                                                                                               06-NOV-1997.
                                   Baculovirus.
                                                                                                                                                                                                                                                                 Borgford T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        component.
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The present invention describes new purified and isolated nucleic acids (II) and anoding: (I) the A and B chains of a ricin-like toxin (II); and (II); and chains linker, joining the two chains and including a cleavage recognition site for a disease-specific protease (III). Also described are: (I) plasmids or baculovirus transfer vectors that contains (I); and (2) recombinant protein (IV) consisting of the A and B Chains of (II) in host cells, are used to inhibit or kill diseased cells that produce (III), particularly for treating cancers (e.g. leucocyte produce (III), particularly for treating cancers (e.g. leucocyte produce (III), particularly for treating cancers (e.g. leucocyte produce (III), particularly for treating cancers (IV) constants or viruses (e.g. infections caused by fungi, parasites (e.g. nalazia) or viruses (e.g. infections caused by though parasites (e.g. nalazia) or viruses (e.g. infections caused by ting), is used to express and multiple solionyelitis or varicella zoster), also cystic fibrosis and multiple calcincity on a cell-binding component. When used to treat viruses component in from endoplasmic reticulum to cytoplasm (which some seption to avoid immune detection), so eslectivity and safety are further improved. (IV) are not toxic until chain A is released and this occurs only in target cells. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7002 accraarcarcarcaraccrerrrecrereraaarrerrarcecreacaarrecaear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711 ACGIRATCAIGGICAIAGCIGITICCIGIGIGAAAITGITAICCGCICACAAITCCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding ricin-like toxin with an interchain linker cleaved by protease - is specific for diseased cells, useful for, e.g. killing selectively cancer or infected cells
                                                                      Ricin-like toxin, cancer, viral infection, parasitic infection, linker, B chain; A chain; protease, fungal infection; malaria; leucocyte proliferation; cytomegalovirus; herpes; hepatitis; rhinovirus; laryngeotracheitis; poliomyelitis; varicella zoster; cystic fibrosis; multiple sclerosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%; Score 291; DB 20; Length 9632; 100.0%; Pred. No. 2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9632 BP; 2602 A; 2122 C; 2176 G; 2732 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                       Baculovirus transfer vector pVL1393 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. A...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  97US-0063715.
97US-0045148.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (DNOV-) DE NOVO ENZYME CORP.
                                                                                                                                                                                                                                                                                                                                            98WO-CA00394
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-009431/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                              WO9849311-A2
                                                                                                                                                                                                                                                                                                                                          30-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1997;
  15-APR-1999
                                                                                                                                                                                                                                                                                                     05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borgford T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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This sequence is a fragment of the pUC 18 nucleotide sequence. The fragments is used in the course of the invention. The invention relates to pyrrole derivatives which recognise a specific DNA base sequence, and strongly bind to the adjacent base via a covalent bond. The pyrrole derivatives alkylate the base sequence, once it has been recognised. The invention also relates to an agent (made from the pyrrole derivatives) for alkylating genes, a process for producing an agent for alkylating genes, and a method for regulating the expression of a gene with a part containing the specific base sequence comprising using an alkylating agent. The compounds are useful in drug compositions for regulating expression of a gene carrying a base sequence which can be recognized then alkylated by them, e.g. in treatment of cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrrole derivative; DUC 18; alkylating agent; gene expression regulator; treatment; drug; cancer; ds.
                                                                                                                                                                         CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                                                                                                                         ATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
                                        106 ceraarcareercaraecrerrrecrereraaarrerrareeecreaarrecaeaa
                                                                                                                             ATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                                                                    New pyrrole derivatives for alkylating specific base sequence of DNA, useful in drug compositions for regulating expression of a gene carrying a base sequence which can be recognized then alkylated by them, e.g. in treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                      ceregereacteaerecerecerecerecerrecerecerecesecena 1001
                                                                                                                                                                                                                                                                                                                                                                                           ccircectrachactracharactracharactracactracacacacan 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragment #2 of pUC 18 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 29; 35pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISC-) JAPAN SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    宙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-JP01228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA10990 standard; DNA; 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200015641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                              832
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                                                                                                                                                                                                                                                                     892
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                            7182 CATTAATGAATCGGCCAACGCGGGGGGGGGGGTTTGCGTATTGGGCGCTCTTCCGCT 7241
    7122 ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG 7181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, prostate cancer, cytostatic; carcinogen, pharmacodyanamic marker, pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                   CATTAATGAATCGGCCAACGCGGGGGGGGGCGGTTTGCGTATTGGGCGCTCTTCCGCT

    is also useful as a pharmacodyanamic or pharmacogenomic marker

                                                                                                                                                                7242 TCCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGCGGCGGCGGGTA 7292
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                                                                                                                                                                                                                                                                                                                                                                                                                               prostate expression marker cDNA 45284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 8964; 11750pp; English
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                                                                                                                                                                                                                                                                                                  ABV45293 standard; cDNA; 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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18-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                          ABV45293;
                                                   891
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29.0%; Score 290; DB 21; Length 450;

Query Match

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Gaps

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                                                                                                                                                832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 891
                                                                                                                                                                                                                                                 198 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGGGGCAGCTGC 257
                                                                                                                                                                                                                                                                                              892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
                                                                                                                                                                                                                                                                                                                                   258 ATTAATGAATCGGCCAACGCGGGGGAGAGGGGGTTTGCGTATTGGGCGCTCTTCCGCTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAAB1453 to AAAB2114 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAAB1260 to AAAB1303 and AAB25620 to AAB2563 represent Neisseria DNA sequences and their corresponding proteins; AAAB1254 to AAAB1259 and AAAB1304 to AAAB1321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1252 special second because of Neisseria meningitidis Memb Polymucleoride ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies
                                                                       712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAQAATTCCAQAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tettelin H, Venter JC;
Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                                       952 CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 1001
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Pred, No. 1.2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 1653; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frazer CM, Hickey E, Peterson J,
Masignani V, Galeotti C, Mora M,
Rappuoli R, Pizza M;
1 '0 '80.00T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA82004 standard; DNA; 515 BP.
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                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
            Best Local Similarity
Matches 290; Conserv
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30-APR-1999;
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composition can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to composition due to be reserved by acteria. For example, some of the identified proteins could be components of vaccines against Meningococus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences of components and last of actilitate production of biological probes, particularly organism specific probes. Attempts to make efficacious Meningococus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequence may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
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                                                                                                                                                                                                                                                                                                                                                                                                             771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892 ATTAATGAATCGGCCAACGCGCGCGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                             712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                               212 CGTAATCATGGTCATAGCTGTTTCCTGTGAATTGTTATCCGCTCACAATTGCACACA
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                                                                                                                                                                                                                                                                                                   Sequence 515 BP; 110 A; 129 C; 122 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   29.0%; Score 290; DB 21;
100.0%; Pred. No. 1.2e-80;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 45299.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
9-UUN-2000; 2000US-21314P.
18-UUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                           290; Conservative
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              831
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                                                                                                                                                                                                                                                                                                                                                                      in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(f) assessing whether prostate cancer has metastasized in a patient;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                      (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lung tumour protein related nucleotide sequence SEQ ID NO:639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                952 CCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 561 BP; 126 A; 146 C; 159 G; 130 T; 0 other;
                                                                                                                                                                Claim 1; Page 8966; 11750pp; English.
  Monahan JE;
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Best Local Similarity 100.0
Matches 290; Conservative
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Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                    cancer in a patient;
                                        WPI; 2001-662795/76.
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The present invention describes immunogenic portions of lung tumourassociated proteins (I) and the nucleic acids (NAs) that encode them.

(I) have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumourassociated to proteins they encode may be used in the prevention, treatment and proteins they encode may be used in the prevention, treatment and chagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to creat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (I). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NAs may be used to produce the lung-tumour associated protein and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in cancer. The (I) may be used as antisens in the production of antibodies and in assays to identify modulators (agoniets and antagonists) of the expression and activity of the protein. AAF68083 to AAF68878 and AAB768878 represent human lung tumour protein related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                891
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                                                                                                                                                                                                                                                                                                                                                                                                tumor-associated proteins and the nucleic acids that encode them,
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                                                                                                                                                                                                                                                                                                                                                                                                                       useful for preventing, diagnosing and treating lung cancer
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                                                                                                                                                                                                                                                                                            Lodes MJ, Fanger GR, Vedvick TS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.0%; Score 290; DB 22; Best Local Similarity 100.0%; Pred. No. 1.1e-80; Matches 290; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 360; 436pp; English.
                                                        99US-0419356.
99US-0466867.
99US-0476300.
                                                                                                                      06-MAR-2000; 2000US-0519642.
22-MAR-2000; 2000US-0533077.
27-APR-2000; 2000US-05660465.
57-APR-2000; 2000US-0560408.
05-JUN-2000; 2000US-0589184.
30-JUN-2000; 2000WO-US18061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention.
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Retter MW, Mannion J;
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Best Local Similarity
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Clapper JD;
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(MCNE/)
(CLAP/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for tremoving tumour cells from a biological sample. The polynucleotide is also useful as probe or parimer to detect the level of mRNA encoding a tumour protein fragment, described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                   Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
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                                                                                                  Lung tumcur; cancer; T cell; immune response stimulator; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 584 BP; 142 A; 159 C; 153 G; 130 T; 0 other;
                                                                                 cDNA encoding clone #26843 of lung tumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID No 639; 223pp; English.
                       BP.
                                                                                                                                                                                                                  11-JUL-2000, 2000US-0614124.
29-AUG-2000, 2000US-0651563.
08-SEP-2000, 2000US-065824.
26-SEP-2000, 2000US-0671325.
06-OCT-2000, 2000US-0702705.
13-DEC-2000; 2000US-0702705.
                       ABK38615 standard; cDNA; 584
                                                                                                                                                                                                10-JUL-2001; 2001WO-US22058
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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                                                                                                                                                         WO200204514-A2.
                                                                                                                                                                                                                                                                                                                                 Wang T, Watan
Marnerakis M,
                                                                                                                                    Homo sapiens.
                                                             21-MAY-2002
                                                                                                                                                                             17-JAN-2002
                                          ABK38615;
             ABK38615
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The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence ($2) mentioned in perintial of at least 20 mentioned in complement of $1, sequences consisting of at least 20 contiguous residues of $1, sequences that hybridise to $1, sequences that hybridise to $1, sequences on a sequence that hybridise to $1, sequences on a sequence for a printial and the sequence sequence from any one of the 4 amino acid sequences mentioned in the specification, a sequence encoded by the polynucleotide, or sequence specification, a sequence encoded by the polynucleotide, or sequence of a polynucleotide, or sequence of a polynucleotide, or sequence of a polynucleotide, or sequence of a cancer in a patient, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polypeptide, detecting the presence of a cancer in a patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to $1 under moderately stringent conditions, stimulating and/or expanding T cells with
                                                                   216
                                                                                                                                               951
                                                                                                                                                                                                                  276
                                               157 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                  Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer
332 CATTAATIGGGTIGGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGCCAGCTGC
                                                                                                                                               892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
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FANGER G F
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2000US-0533077. 2000US-0546259. 2000US-0560406.

2000US-0589184. 2000US-0614124. 2000US-0651563.

2000US-0658824 2000US-0671325

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New polynucleotide, useful for preparing a compositinhibiting development of cancer, e.g. lung cancer
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30-0CT-2000; 2000US-0702705.
13-DEC-2000; 2000US-0736457.
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                                                                                                             06-MAR-2000;
22-MAR-2000;
10-APR-2000;
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the polynuclectide, protein or antigen-presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4+ and/or CD8+ T cells isolated from a patient with the polynuclectide, protein or antigen presenting cells that express the copymuclectide, such that T cells proliferated, administering to the patient an effective amount of the proliferated T cells, and thus copymuclectide, protein and calcer in the patient. The inhibiting the development of a cancer in the patient. The composition for stimulating an immune response in a patient, and for treating a cancer in catedral and correcting a useful for determining the presence of a cancer). The oligonuclectide is useful for coligonuclectide are useful in pharmaceutical compositions, e.g. vaccines. The polynuclectide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of proteins in tumour cells. An amplified portion of the polynuclectide is full length, extended or patial) is calated from a library derived from lung tumour/cancer cells.

Con soluted from a library derived from lung tumour/cancer cells.

Con formational direction, but was obtained in electronic form part from a directly from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the USPP from the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       segdata.uspto.gov/sequence.html?DocId=20020197669.
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Durham M;

Johnson JC, Retter MW, Bangur CS, Mcnabb A;

Watanabe Y, Vedvick TS,

RA, Wang T, Fanger GR,

or

composition for treating

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The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer.
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29.0%; Score 290; DB 25; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.1e-80;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                               Sequence 584 BP; 142 A; 159 C; 153 G; 130 T; 0 other;
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Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss. Lung cancer therapyand diagnosis associated cDNA #622.

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10-JUL-2001; 2001US-0902941.

US2002172952-A1. Homo sapiens

21-NOV-2002

Open reading frame; ORF; low stringency; sequencing; ORESTES; bronchitis; identification; internal region; population study; heart disease; Alzheimer's disease; human; ds.

WO200274994-A2.

26-SEP-2002

Homo sapiens

Orestes sequencing method related DNA SEQ ID No 387.

Determining ORFs of the genome by contacting mRNA with a single oligonucleotide primer, useful for population studies that identify genes associated with diseases such as cardiovascular, autoimmune and

Brentani RR;

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Dias-neto

Simpson AJG,

WPI; 2002-750567/81.

congenital diseases

(LUDW-) LUDWIG INST CANCER RES 07-NOV-2000; 2000US-246313P. 01-NOV-2001; 2001WO-US46665.

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Method for determining open reading frames of the genome of an organism using primers at low stringency conditions, useful in the construction of contigs or constructs of sequenced nucleic acid molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a cDNA sequence obtained using a method for determining open reading frames (ORFS) of the genome of an organism. An aliquot of mRNA from human breast cancer cells was mixed with a single, arbitrary primer, Moloney murine leukaemia virus reverse transcriptase, reverse transcriptase buffer and GNTPs. The mixture was incubated under low stringency conditions to yield single stranded CDNA. The same primer was then used to amplify the cDNA by PCR. Rather than providing nucleotide sequence information from the non-coding the more interesting and relevant internal portions, such as ORFS. The method also permits the construction of contigs of sequenced nucleic
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            cDNA synthesis; contig sequence construction; low stringency; cDNA sequencing; ss.
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                                                                                                                                                                                                                                                                          Brentani RR;
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Page 112; 113pp; English.
                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
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                Human; arbitrary primer;
open reading frame; ORF;
                                                                                                                                                                                                                                                                                                            WPI; 2000-400100/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 290; Conserv
                                                                                                    WO200031299-A2
                                                                                                                                                                      19-NOV-1999;
                                                                    Homo sapiens
                                                                                                                                                                                                         20-NOV-1998;
                                                                                                                                     02-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frames (ORFS) of the genome of an organism comprising contacting messenger RNA from a cell of the organism with a single, oligonucleotide primer at low stringency. The method is an improved ORBSTS sequencing method. The methods of the present invention are useful for sequencing of, essentially, the entire coding component of an organism, identification of previously unknown nucleic acid molecules, assigning previously identified nucleocide sequences to internal regions of genes and population studies that identify genes associated with diseases such as heart disease, bronchits, Alzheimer's disease, autoimmune diseases and congenital diseases. This polynucleotide represents a DNA sequence that is used in the novel method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 ATTAATGAATCGGCCAACGCGGGGGAGAGGCGGTTTGCGTATTGGGCGCTTTTCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 CATTAATTGCGTTGCGCTCACTGCCCCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for determining open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 15, 2004, 22:40:26 Job time : 327.065 secs
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Matches 290; Conservative
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ABT12681 standard; DNA; 598

RESULT 15

(first entry)

02-JAN-2003

ABT12681;

ABT12681 ID ABT1 XX AC ABT1 XX DT 02-

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Sequence 1, Appli
Sequence 639, Appli
Sequence 639, App
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
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                                                                                February 15, 2004, 10:22:55; Search time 73.6147 Seconds (without alignments) 6001.851 Million cell updates/sec
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1. /cgn2 6/ptodatca/2/ina/5a_COMB.seq:*

2. /cgn2 6/ptodatca/2/ina/5a_COMB.seq:*

3. /cgn2 6/ptodatca/2/ina/6a_COMB.seq:*

4. /cgn2 6/ptodatca/2/ina/Ba_COMB.seq:*

5. /cgn2 6/ptodatca/2/ina/PCTUS COMB.seq:*

5. /cgn2 6/ptodatca/2/ina/PCTUS COMB.seq:*

5. /cgn2 6/ptodatca/2/ina/PCTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-702-705-639
US-08-706-705-24
US-08-706-706-24
US-08-706-706-24
US-08-706-702-26
US-08-706-702-26
US-08-706-702-26
US-08-998-411-25
US-08-998-411-25
US-08-998-411-25
US-08-998-411-25
US-08-98-471-25
US-08-706-706-25
US-08-706-706-25
US-09-228-471-25
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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US-08-417-226-9
                                                                                                                                         US-09-921-143-36_COPY_2000_3000
                                                                                                                                                                                                                                        569978 segs, 220691566 residues
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                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                              OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                     Word size :
                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                        Searched:
                                                                                 Run on:
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RESULT 1
US-08-155-888-1
i Sequence 1, Application US/08155888
sequence 1, Application US/08155888
sequence 1, Application Stephen L.
APPLICANT: Hoffinan, Richard C.
APPLICANT: Sedegah, Martha C.
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINE
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
TITLE OF INVENTION: DELIVERING POLYNUCLEOTIDE VACCINES
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Naval Medical Res. & Dev. Cmd.
STREET: Baldg: 1, T-12 8901 Wisconsin Ave.
CITY: Betheeda
STRIEE: Maryland
COUNTRY: USA
STRIE: Maryland
COUNTRY: USA
STRIEE: VARDABLE FORM:
                                                                                   Sequence 6, Appli
Sequence 17, Appl
Sequence 11, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 9, Appendix Sequence 7, Appendix Bequence 6, Appendix Bequence 17, Sequence 11,
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
US-09-196-131-9
US-08-641-732-9
US-07-016-0982-9
US-08-446-935-6
US-09-401-171C-11
US-09-401-171C-11
US-09-503-222-6
US-09-675-019-8
US-09-075-019-8
US-09-075-019-8
US-09-173-053-4
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US-09-00-2315-113-5
US-09-00-2315-113-3
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IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="promoter"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /label=CMV-IE
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NAME: Spevack, A. David.
NAME: Spevack, A. David.
REGISTRATION NUMBER: 24, 743
REFERENCE/DOCKET NUMBER: N.C. 75,851
RELEPHONICATION INFORMATION:
FILEPHONICATION INFORMATION:
FILEPHONICATION INFORMATION:
FILEPHONICATION INFORMATION:
FILEPHONICATION INFORMATION:
FILEPHONICATION INFORMATION:
FILEPHONICATION: 295-6159
FILEPHONICATION: 295-6169
FILEPHONICATION: 1:
SEQUENCE CHARACTERISTICS:
FIRANDENESS: double
FIRANDENESS: double
FIRANDENESS: double
FILEPHONICATION INFORMATION:
FILEPHONICATION INFORMATION IN
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      HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: NAMES (RRY: promoter Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Comm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2759 CTIGICICACAGCCAIGCAACCCIIGCCICCIGIGCIGACTIAGCAGGGGAIAAAGIGAG 2818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2819 AGAAAGCCTGGGCTAATCGGGGGCTCGCTCCTCCTAACTGGATTGTCCTATGTGT 2878
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LOCATION: 933..2367
LDENTIFICATION METHOD: experimental
OTHER INFORMATION: (codon start= 933
OTHER INFORMATION: (function= "protein protective against malaria"
OTHER INFORMATION: (function= "protein"
OTHER INFORMATION: (Authore= "protein"
OTHER INFORMATION: (Authore= 1 EXPERIMENTAL
OTHER INFORMATION: (Authore= 1 EXPERIMENTAL
OTHER INFORMATION: (Authore= (1])
DUBLICATION INFORMATION: (Atation= (1])
AUTHORS: Sedegah, martha
AUTHORS: Hedstrom, Richard C.
AUTHORS: Hoffman, Stephen L.
TITLE: Vacchaation with Plasmodium yoelii CS protein
TITLE: plasmid DNA protects against malaria
JOURNAL: Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 CTTGTCTCACAGCCATGCAACCCTTGCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAG 290
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/note= "This feature acts as a promoter for any
downstream DNA sequence."
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5552;
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30.7%; Score 307; DB 3; Length 55:
Best Local Similarity 99.3%; Pred. No. 1.9e-112;
Matches 457; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Cullen, Bryan R.
TITLE: TRANS-ACTIVATION OF HUMAN IMMUNODEFICIENCY
TITLE: VIRUS OCCURS VIA A BIMODAL MECHANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 26 SEP-1986
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 4732
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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US-09-486-336A-2
                                                                           FEATURE:
NAME/KEY:
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; Sequence 2, Application US/09486336A; Patent No. 6566336

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258 ATTAATGAATCGGCCGAACGCGGGGGGGGGGGTTTGCGTATTGGGCGCTCTTCCGCTT 317
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                                                                          APPLICANT: SAITO, ISA

TITLE OF INVENTION: A COMPOUND TO ALKYLAUE FOR THE SPECIFIC
TITLE OF INVENTION: A COMPOUND TO ALKYLAUE FOR THE SPECIFIC
TITLE OF INVENTION: SEQUENCE IN DNA AND ITS METHOD OF PREPARATION
FILE REPERENCE: 49430 (71526)
CURRENT APPLICATION NUMBER: US/09/486,336A
CURRENT PAPLICATION NUMBER: POT/JP99/01228
PRIOR RYLING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FREESEQ FOR Windows Version 3.0
SEQ ID NO 2
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952 CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 1001
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APPLICANT: Rannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE TELE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.0%; Score 290; DB 4; Length 450; 100.0%; Pred. No. 1.6e-105; tive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 639
LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 639, Application US/09702705; Patent No. 6504010; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vadvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Hiroshi
APPLICANT: TAO, Zhi Fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 290; Conservative
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US-09-702-705-639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: pUC 18
US-09-486-336A-2
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US-09-702-705-639
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952 CCTCGCTCACTGACTCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY; both
; MOLECULE TYPE: DNA (genomic)
US-08-706-702-24
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EDNESS: both
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                                                                                                        RESULT 5
US-08-706-702-24
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                                                                                                                                                                                                                                                                                                                                                                        217 ATTAATGAATCGGCCCAACGCGCGGGAGAGGCGCTTTGCGTTTGCGCGCTCTTCCGCTT 276
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                                                                                   712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA 771
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                                                                                                                           37 ceraarcareercaracererricererereaaarrerreecereacaarrecacaca 96
                                                                                                                                                                       0; Gaps
                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILICATION DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 326
Query Match 29.0%; Score 290; DB 4; Length 584; Best Local Similarity 100.0%; Pred. No. 1.5e-105; Matches 290; Conservative 0; Mismatches 0; Indels
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29.0%; Score 290; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-105;
Matches 290; Conservative 0; Mismatches 0;
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Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Tongtong
Bangur, Chaitanya S.
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Rannion, Jane
Fan, Ligun
Wang, Aijun
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US-09-736-457-639
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LENGTH: 584
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA 771
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277 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCCGCGAGCGGTA 326
                                                                                                                                                Sequence 24, Application US/08706702

Ratent No. 594814

GENERAL INFORMATION:

TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga
TITLE OF INVENTION: maritima and Mutants Thereof
NUMBER OF SEQUENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCES: 3FERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600

CITY: Machington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 701;
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Best Local Similarity 100.0%; Pred. No. 1.5e-105;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:

COUNTRY:

COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EMP C compatible
CORFUTER: EMP C compatible
CORFUTER: EMP C COMPACTION
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,702
FILING DATE: 0-SEP-1996
CLASSIPFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.2800006
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATE:
TILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
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US-09-238-471-24
US-08-706-706-24
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                                    167 CATTAATIGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 226
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                                                                                                                                                                                                                227 ATTAATGAATCGGCCAACGCGCGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 286
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Batent No. 6015668

GENERAL INFORMATION:
APPLICANT: Hughes, A. John
APPLICANT: Chatteriee, Deb K.
TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES. 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CLTY: Washington
                                                                                                                                                                                                                                                                                                                                           287 CCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGGCGAGCGGTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: UGA

ZIP: 20005-3934

ZIP: 20005-3934

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/69,807
FILING DATE: 06-SEP-1996
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/637,400
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/537,400
FILING DATE: 01-JAN-1995
PRICK APPLICATION NUMBER: US 08/537,400
FILING DATE: 01-JAN-1995
PRICK APPLICATION NUMBER: US 08/37,400
FILING DATE: 10-JAN-1995
PRICK APPLICATION NUMBER: US 08/37,337
FILING DATE: 10-JAN-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/37,337
FILING DATE: 10-SEP-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/56,759
FILING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
FILING DATE: 11-DEC-1995
FILING DATE: 01-DEC-1995
FILING DATE: 0
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REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET UNBER: 094
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 24:
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LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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US-08-706-706-24
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Patent No. 6506560

GENERAL INFORMATION:

APPLICANT: Hughes, A. John
Chatterjee, Deb K.

TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               952 CCTCGCTCACTGACTCGCTGCGCTCGTTCGGCTGCGGCGAGCGGTA 1001
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CORRESPONDENCE ADDRESS:
ADDRESSES: STEREN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
Query Match 29.0%; Score 290; DB 3; Length 701; Best Local Similarity 100.0%; Pred. No. 1.5e-105; Matches 290; Conservative 0; Mismatches 0; Indels
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MEDLUM TYPE: RIOPPY disk

COMPUTER: INDEPT Compatible

COMPUTER: INDEPT COMPATIBLE

COMPUTER: INDEPT COMPATIBLE

COMPUTER: INDEPT COMPATIBLE

COMPUTER: INDEPT COMPATIBLE

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APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-DEC-1995
APPLICATION NUMBER: US 08/537,397
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STATE: DC
COUNTRY: USA
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US 08/537,397

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Patent No. 5498614
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
TITLE OF INVENTION:
TITLE OF INVENTION: anaitima and Mutants Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
                                                                                                                                                                                                                                                                                                                  Query Match 29.0%; Score 290; DB 4; Length 701; Best Local Similarity 100.0%; Pred. No. 1.5e-105; Matches 290; Conservative 0; Mismatches 0; Indels
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STATE: DC
COUNTRY: USA
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE PORM:
MEDIUM TYE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PREENT PC DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,702
FILING DATE: 06-SEP-1996
FILING DATE: 06-SEP-1996
TILING DATE: NG-SEP-1996
TILING DATE: NG-SEP-1996
TILING DATE: NG-SEP-1996
TILING DATE: NG-SEP-1996
                                                                                                                                                                     TOPOLOGY: both

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-238-471-24
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APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
PRICA APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-0CT-1995
FRICA APPLICATION DATA:
FRICA APPLICATION DATA:
APPLICATION UNMER: US 08/576,759
FRICA APPLICATION DATA:
APPLICATION UNMER: US 08/576,759
FRILNG DATE: 21-DEC-1995
PRICA APPLICATION DATA:
             TELEFAN. 202-371-2500
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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US-08-706-702-26
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Retent No. 6015668

GENERAL INFORMATION:
APPLICANT: Hughes, A. John
APPLICANT: Claned DNA Polymerases from Thermotoga and
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STRRET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 CCTCGCTCACTGACTCGCTCGCTCGGTCGTCGCTGCGCGAGCGGTA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%; Score 290; DB 2; Length 71.
ilarity 100.0%; Pred. No. 1.4e-105;
Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDDUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/706, 706

FILING DATE: 06-SEP-1996

CLASSIPTCATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/689,807
                                                                                                                                           NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERNICE/DOCKET NUMBER: 0942.2800006
TELECOMMINICATION INFORMATION:
TELEPHONE: 202-371-260
               FILING DATE: 02-00T-1995
PRIOR APPLICATION NUMBER: US 08/525,057
PTLING DATE: 08-5EP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
US-08-706-702-26
                                                                                                                                                                                                                                                                                                                                      : 713 base pairs
nucleic acid
EDNESS: both
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   both
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US-08-706-706-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0942.2800005
FILING DATE: 14-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/370,190
FILING DATE: 01-CAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
PRIOR APPLICATION NUMBER: US 08/576,759
FILING DATE: 02-OCT-1995
PRIOR APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
PRIOR APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ESHOOID, ROBERT 32,893
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 09.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 CAFTAATTGCGFTGCCCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 ATTAATGAATCGGCGAAAGGCGGGGGGGGGTTTGGGGTATTGGGCGCTCTTCGGCTT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  892 ATTAATGAATCGGCCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   832 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,471
FILING DATE: SS-Jan-1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-077-1995
FILING DATE: 02-077-1995
FILING DATE: US 08/370,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/316,423
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: US 08/576,759
FILING DATE: 21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-0CT-1995
APPLICATION NUMBER: US 08/525,057
FILING DATE: 08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-238-471-26
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RESULT 11 US-08-998-416-55

Segrence 26, Application US/09238471
Fatent No. 550550
GENERAL INFORMATION:
APPLICANT: Hughes, A. John
ITILE OF INVENTION: Clanterjee, Deb K.
ITILE OF INVENTION: Claned DNA Polymerases from Thermotoga and NUMBER OF SEGUENCES: 26
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington

US-09-238-471-26

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RESULT 12
US-08-706-702-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 385
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                                                               APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Juxgen
APPLICANT: Wenchile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET; 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952 CCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTA 1001
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Best Local Similarity 100.0%; Pred. No. 1.4e-105;
Matches 290; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meige, U TIMOCHY
REGISTRATION NUMBER: BF/5-30306/A/CGC1976
TELEPRATION NUMBER: BF/5-30306/A/CGC1976
TELEPRATION NUMBER: BF/5-30306/A/CGC1976
TELEPRAX: 919-541-8689
INPORMATION ES SEQ ID NO: SE:
FEMALTION FOR SEQ ID NO: SE:
FEMALTION FOR SEQ ID NO: SE:
FEMALTION FOR SEQ ID NO: SE:
FEMALTION FOR SEQ ID NO: SE:
FEMALTION FOR SEQ ID NO: SE:
FEMALTION TO BE DAILS
Sequence 55, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: PAG1015UP
US-08-998-416-55
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MOLECULE TYPE: DO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 27709
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REBELL 1. 10.25

Sequence 2. Application US/09706702

Sequence 2. Application US/09706702

Sequence 2. Application US/09706702

SERVICANT Consteries Deb K.

TITLE OF INVENTION:

NUMBER OF INVENTION:

ADDITION OF SEQUENCES: 36

ADDITION OF SEQUENCES: 36

ADDITION OF SEQUENCES: 36

ADDITION OF SEQUENCES: 36

ADDITION OF SEQUENCES: 36

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                                   265 ATTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 324
892 ATTAATGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
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                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08706706

Patent No. 6015668

GENERAL INFORMATION:
APPLICANT: Hughes, A. John
APPLICANT: Charterjee, Deb K.
TILE OF INVENTION: Cloned DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY, Machington
                                                                                                                                      325 CCTCGCTCACTGACTCGCTGCGCTCGTCGTTCGGCTGCGGCGGTA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPOTER: IBM PC COMPALIBLE
COMPARE: IBM PC COMPALIBLE
COMPARE: PATENTIN Felease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/689,807
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/689,807
FILING APPLICATION DATA:
APPLICATION PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: US 08/689,807
FILING APPLICATION DATE: US 08/689,807
FILING APPLICATION DATA:
AND TAXATON WINNER: US 08/689,807
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FILING DATE: 02-007-1995
FILING APPLICATION DATA: US 08/370,190
FILING DATE: 01-07N-1995
FILING DATE: 01-07N-1995
FILING DATE: 30-589-1994
FILING DATE: 30-589-1994
FILING DATE: 21-050-1995
FILING DATE: 21-050-1995
FILING DATE: 21-050-1995
FILING DATE: 02-007-1995
FILING DATE: 02-007-1995
FILING DATE: 02-007-1995
FILING DATE: 02-007-1995
FILING DATE: 03-589-1995
FILING DATE: 03-589-1995
FILING DATE: 03-689-1995
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TELEPHONE: 202-371-260
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                both
PE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE:
US-08-706-706-25
                                                                                                                                                                                                                                                                US-08-706-706-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D
COUNTRY:
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29.0%; Score 290; DB 3; Length 717;

Query Match

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                                                                                                                                                                                                      832 CATTAATIGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 ATTAATGAATGGGCCAACGCGGGGGGAGAGGGGGTTTGCGTATTGGGCGCTCTTCCGCTT 324
                                                                                                                                                                                                                                                                                                                                                                           205 CATTAATTIGGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                       892 ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT 951
                                                                                        712 CGTAATCATGGTCATAGCTGTTTCCTGTGAAATTGTTATCCGCTCACAATTCCACACA
                                  0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-238-471-25
; Sequence 25, Application US/09238471
; Sequence 25, Application US/09238471
; GENERAL INPORMATION:
    TITLE No. (Sequence)
; TITLE OF INVENTION: Cloud DNA Polymerases from Thermotoga and NUMBER OF SEQUENCES: 26
; CORRESPONDENCES: 26
; CORRESPONDENCE ADDRESS:
    STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA 1001
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MEDIUTY TYEE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 28-Jan-1999
CLASSIFICATION: «Unknown»
ilarity 100.0%; Pred. No. 1.4e-105;
Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US 08/537,397
FILING DATE: 02-OCT-1995
APPLICATION NUMBER: US 08/525,057
FILING DATE: 08 -SER-1995
ATTORNEY AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 23,893
REFERENCE/DOCKET NUMBER: 0942.2800005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,706
FILING DATE: 06-SEP-1996
APPLICATION NUMBER: US 08/689,807
FILING DATE: 14-AUG-1996
APPLICATION NUMBER: US 08/537,400
FILING DATE: 02-OCT-1995
APPLICATION NUMBER: US 08/370,190
FILING DATE: 01-JAN-1995
APPLICATION NUMBER: US 08/316,423
APPLICATION NUMBER: US 08/316,423
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APPLICATION NUMBER: US 08/576,759
   Best Local Similarity
Matches 290; Conserv
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712 CGTAATCATGGTCATAGCTGTTTCCTGTGGAAATTGTTATCCGCTCACAATTCCACA 771
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                                                                                                                                                                                                                                                          Length 717;
                                                                                                                                                                                                                                                       Query Match 29.0%; Score 290; DB 4; Length 717 Best Local Similarity 100.0%; Pred. No. 1.4e-105; Matches 290; Conservative 0; Mismatches 0; Indels
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Patent No. 5800996

GENERAL INFORMATION

PERKIN-Elmer Corporation, Applied Biosystems APPLICANT: Division

TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED TITLE OF INVENTION: FUUCRESCENCE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
ADDRESSEE: & Rosati
STREET: 650 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1050
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTE: 1BM compatible
OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
SOTWARE: MOrdperfect for windows 6.0,
SOFTWARE: ASCII (DOS) TEXT format
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/726,462B
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1.17 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
MOLECULE TYPE: DAN (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-238-471-25
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/642,330
FILING DATE: May 3, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/672,196
FILING DATE: June 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: David J. Weitz
RESISTRATION NUMBER: 38,362
REFERENCE/DOCKET NUMBER: PELM4304
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STATE: California
COUNTRY: USA
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US-08-726-462B-3
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229 CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC 288
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                    TELEPHONE: (415) 493-9300
| TELEPAX: (415) 493-6811
| INFORMATION FOR SEQ ID NO: 3:
| SEQUENCE CHARACTERISTICS:
| TENCH: 78 nuclecties
| TYPE: nucleic acid STRANDENNESS: single
| STRANDENNESS: single
| TOPOLOGY: linear
TELECOMMUNICATION INFORMATION:
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Sequence 36, Appl
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2. (Gnn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3. (Ggn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3. (Ggn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3. (Ggn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
3. (Ggn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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3. (Ggn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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4. (Ggn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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4. (Ggn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-01-394-511-1
US-09-796-692-3110
US-10-15-48818-3110
US-10-15-48818-3110
US-10-270-89-103
US-10-270-89-103
US-10-15-48818-3746
US-10-15-48818-3746
US-10-15-48418-3746
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US-10-15-48418-3746
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US-10-15-48418-39
US-09-902-941-639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                        Run on:
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		Quer Best Matcl	Query Match Best Local Si Matches 1001,	Similarity 1; Conser	100.09 y 100.09 rvative		; Score ; Pred. 0; Misn	e 1001; No. 0 smatche	·- 0	DB 13; Length 0; Indels	th 5283; s 0;	Gaps	0,	
	о п	දු දු			TAACCAG TAACCAG	55-F	GGGCACA1 GGGCACA1	F - F	7.07.00 	GCAGCTAGAC	4-4	ATGGT ATGGT	60 2059	
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2060 AGCTGCCAGGAAGGAAGTGAGAATCCTTCCTTAAGTCTCCTAGGTGGTGAGGGGGGCTAG

61 AGCTGCCAGGAAGGAGTGAGAATCCTTACTTAAGTCTCCTAGGTGGTGACGGGGGGGCTAG 120

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901 TCGGCCAACGCGCGGGGGAGGCGGTTTGCGTATTGGCGCTCTTCCGCTTCTCGCTCA 960
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                                                                                                                             2240 AGCCATGCAACCTTGCCTCCTGTGCTGACTTAGCAGGGATAAAGTGAGAAAAAAAGCCTG 2299
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GURREAL INDOMANTION:
APPLICANT: Algaete, Paul A.
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APPLICANT: Algaete, Paul A.
APPLICANT: Algaete, Paul A.
APPLICANT: Algaete, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERE
TITLE OF INVENTION: COMPOSITION AND THE TOTAL OF THE TOTAL NUMBER: US 0/01-01-01
PRIOR PELICATION NUMBER: US 0/01-03-01
PRIOR PELING DATE: 2000-03-01
PRIOR PELING DATE: 2000-04-22
PRIOR APPLICATION NUMBER: 0/220, 303
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PRIOR PLING DATE: 2000-05-01
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; OTHER OCHATION: Baculovirus transfer vector pVL1393
US-10-394-511-1
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Publication No. US20020198362A1
GENERAL INFORMATION:
                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 9632
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Composition and Methods for the Detection, Diagnosis and Thera
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and TILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and THERE CONTRACT FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,479
PRIOR FILING DATE: 2000-04-27
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Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps
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ORGANISM: Homo sapiens
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    ; SEQ ID NO 3110
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LENGTH: 380
                                                                                  TYPE: DNA ORGANISM: 1
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APPLICANT: Adagate, Paul A.
APPLICANT: Adagate, Paul A.
APPLICANT: Clapper, Jonathan David
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APPLICANT: Carter, Lauren
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29.0%; Score 290; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels 0; Gaps
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                         TYPE: DNA
CRGANISM: Homo sapiens
US-09-796-692-3110
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APPLICANT: Chao, Qimin
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APPLICANT: Grasso, Luigh
APPLICANT: Sas, philip M.
APPLICANT: Sas, philip M.
APPLICANT: Nicolaides, Nicholas C.
TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagno TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagno CURRENT PLING PATER: 2002-10-11
CURRENT FILING DATE: 2002-10-12
PRIOR FILING DATE: 2001-10-12
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SEQ ID NO 103
LEASTHARE: PARENTIN VERSION 3.1
SEQ ID NO 103
LEASTHARE: AMERITIN VERSION 3.1
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                                                                                                                               Length 380;
                                                                                                                                                                                                         0; Indels
                                                                                                                      Query Match
29.0%; Score 290; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0;
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Conservative 0; Mismatches
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    ; ORGANISM: Homo sapiens
US-10-040-862-3110
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APPLICANT: Algate, Faul A.
APPLICANT: Algate, Faul A.
APPLICANT: Mannion, Jame
APPLICANT: Retrier, Marc
APPLICANT: Retrier, Marc
APPLICANT: Retrier, Marc
TILLE OF INVENTION: Lompositions and Methods for the Detection, Diagnosis and Therapy
FILE SPERSHOR: 014058-01522003
CURRENT FILING DAME: 2001-11-06
PRIOR PRICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
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PRIOR PRILING DAME: 2000-0-0-10
PRIOR PLING DAME: 2000-0-12
PRIOR PLING DAME: 2000-0-14
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Sequence 3110, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
US-10-154-884B-3110
                                                                                      Query Match
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APPLICANT: Algate, Paul.
APPLICANT: Algate, Paul.
APPLICANT: Algate, Paul.
APPLICANT: Clapper, Jonachan David
APPLICANT: Clapper, Jonachan David
APPLICANT: Clapper, Jonachan David
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Generalidos and Methods for the Detection, Diagnosis and Theri
TITLE OF INVENTION: Generalidos and Malignancies
TITLE OF INVENTION: Generalidos and Malignancies
TITLE OF INVENTION: Generalidos and Malignancies
TITLE OF INVENTION: MARRER: US 60/20,475
CURRENT FILING DATE: 2000-30-01
PRIOR FILING DATE: 2000-42-2
PRIOR FILING DATE: 2000-44-28
PRIOR FILING DATE: 2000-44-28
PRIOR FILING DATE: 2000-64-28
PRIOR PILING DATE: 2000-64-28
PRIOR PILING DATE: 2000-64-28
PRIOR PILING DATE: 2000-65-01
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PRIOR APPLICATION NUMBER: US 60/206,201
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29.0%; Score 290; DB 12; L
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0;
                                                                                                                                                                                                           Sequence 3746, Application US/10057475B Publication No. US20040002068A1 GENERAL INFORMATION:
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NAME/KEY: misc feature

LOCATION: (1)...(557)

OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-3746
                                                                                                                                                                                                                                                                                                                              APPLICANT: Gaiger, Alexander
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gaiger, Paul A.
APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/180,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,003
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,003
PRIOR APPLICATION NUMBER: 60/202,003
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,303
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
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US-09-796-692-3746
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Matches 290;
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LENGTH: 557
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APPLICANT: Reter, Mannen, Jame
APPLICANT: Reter, Marc
APPLICANT: Reter, Marc
APPLICANT: Reter, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther.
TITLE OF INVENTION: Hematological Malignancies
CURRENT FILING DATE: 2001-11-06
FRIOR APPLICATION NUMBER: US/0/040,862
CURRENT FILING DATE: 2001-03-10
FRIOR APPLICATION NUMBER: US 60/190,479
FRIOR PILING DATE: 2000-04-28
FRIOR PILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
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189 ATTAATGAGCCAACGCGGGGGGAGAGCGGTTTGCGTATTGGGCCCTCTTCGCTT 248
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                                                                                                                                                                                                                                       Sequence 3746, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
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COCATION: (564)
COTHER INFORMATION: n=A,T,C or G
US-10-040-862-3746
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US-10-040-862-3746
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     189 ATTAATGAGCCAACGCGCGGGGAGAGGGGGGTTTGCGTATTGGGGCGCTCTTCCGCTT 248
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                                                                                                                                                                                                                                         ; Sequence 3746, Application US/10154884B; Publication No. US20040005561A1
; GENERAL INFORMATION: APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: (1)...(557)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-3746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 290; Conservative
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US-10-154-884B-3746
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Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 290; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
 CATTAATTGCGTTGCGCTCACTGCCCGCT
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Patent No. US20020172952A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                 Wang, Tongtong
Bangur, Chaltanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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ORGANISM: Homo sapien
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US-09-736-457-639
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ENGTH: 584
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APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Congrong
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
APPLICANT: McNeill, Patricia
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APPLICANT: McNeill, Patricia
APPLICANT: SIONION: DIAGNOSITIONS NUMBER: US/09/849,626
CURRENT PILLING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 639
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                                                      APPLICANT: Retter, Marc W.

APPLICANT: Carter, Marc W.

APPLICANT: Carter, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Wordick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.14.7480.7

CURRENT APPLICATION NUMBER: US/09/902,941

CURRENT FILING DATE: 2001.07-10

NUMBER OF SEQ ID NOS: 2002

SOFFWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020197669A1
BERRAL INCRMATION:
APPLICANT: Bangur, Chaitanya
Watanabe, Yoshihiro
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CRGANISM: Homo sapiens
US-09-902-941-639
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ORGANISM: Homo sapien
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                                                         712 CGTAATCAIGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
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FULLICATION NO. US20030125245A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITION COMPOSITION OF TITLE OF INVENTION: US/09/476,300
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 785
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 584
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100.0%; Pred. No. 1.2e-143;
tive 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 1.2e-143; Matches 290; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 290; Conservative
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CORGANISM: Homo sapien
US-09-476-300-639
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US-09-476-300-639
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BF361513 a GG06312.x
AZ254213 a GG06312.x
BF37686 de13f03.x
BF38187 de35f01.x
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(Ibasea to 362)

(Ilifon, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., WashU Xenopus EST project, 1999

Unpublished
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B1937979 de29e08.x
CB859029 H109B01w
B82861 RPCI11-18D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         df08b08.x1 Wellcome CRC pRN3 St13 17 egg animal cap Xenopus laevis cDNA clone IMAGE:3556574 3' similar to SW:CATA_CAMJE Q59296 CATAASE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              AW790424 C01743-F
B83369 RPCI11-13C2
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WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Feat: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
Xenopus laevis
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CB859029
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TA176D09P
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B1937553
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BI940910.1 GI:16255382
RESULT 1
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DEFINITION
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JOURNAL
COMMENT
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AUTHORS
 B1940910 df08b08.x
B1675829 dag61e05.
B1937546 dd92b12.y
AU224539 AU224539
                                                                               2004, 21:50:21 ; Search time 2636.53 Seconds (without alignments) 9227.587 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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11: gb htc:*
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source

FEATURES

BASE COUNT ORIGIN

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WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, E. ellefroid, and A.M. Zorn
(Wellcome/CRC Institute). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Conscrtium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stops: 273.
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/tione="IMAGE:478855"
/tione="IMAGE:478855"
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/tione="IMAGE:478959; subtracted by stage 19-26 animal cap"
/tione="IMAGE:478959; subtracted by stage 19-26 animal cap"
/tione="IMAGE:478959; subtracted and was constructed by N. Carriage according to Nieuwkoop and Faber: Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute).
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Clifton, D., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.
Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bly37546 391 bp mRNA linear EST 18-OCT-2001 dd92b12.yl Wellcome CRC pcDNAI egg Xenopus laevis cDNA clone MAMSE:341758 5' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 CGTAATCAIGGTCATAGCIGTTTCCTGTGTAAATTGTTATCCGCTCACAATTCCACACA 95
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTAATTGCGTTGCGCTCACTGCCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC
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Best Local Similarity 100.0%; Pred. No. 4.4e-136;
Matches 290; Conservative 0; Mismatches 0;
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Xenopus laevis
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B1675829.1 G1:15628736
EST.
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I (base I to 391)

Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Farvey,N., Ritter,E., Jackson,Y., McCann,R., MashU Xenopus EST project, 1999
Unpublished
                                                                                                                                          Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Possible reversed clone: similarity on wrong strand Seq primer: -400P from Gibco High quality sequence stop: 350.

Location/Qualifiers
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                                         Library constructed by N. Garrett, E. ellefroid, and A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center
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; Pred. No. 4.3e-136;
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           est@watson.wustl.edu
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TITLE JOURNAL COMMENT

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Expressed Sequence Tags from Reproductive Organs of Ipomoea trifida cDNA Libraries
Unpublished
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1 (Dases 1 to 401)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
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dag61g01.y1 Wellcome CRC pRN3 St19 26 egg animal cap Xenopus laevis cDNA clone IMAGE:4785984 5' similar to TR:Q44068 Q44068
ALPH-HEMOLYSIN. ;, mRNA sequence.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Unpublished
Contact: Sandy Clifton, Ph.D.
WashU Kanopus EST project, 1999
WashU Kanopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Ipomoea trifida"
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/downe="Isx-0348"
/tissue_type="stigma"
/dev_erage="tri-nucleate pollen stage"
/clone_lib="Ipomoea trifida stigma"
a 107 c 109 g 102 t
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                                                                                                                                         Contact: Tohru Tsuchiya
Faculty of Bioresources
Mie University
1515 Kamihama, Tsu, Mie 514-8507, Japan
Tel: 81-59-231-9515
Fax: 81-59-231-9515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                      Email: tsuchiya@bio.mie-u.ac.jp.
Location/Qualifiers
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                                                                                       Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashUngton University School of Medicine
WashUngton University School of Medicine
#444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon, (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Manopus clones from this library are available
through the I.M.A.G.E. Consertium/LLML at: info@image.llnl.gov
High quality sequence stop: 367.
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were oligo-dT primed and directionally cloned. Library was
constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute)."

102 c 105 g 89 t 2 others
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Ipomoea trifida cDNA clone ISM-0348
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1 (Dasea 1 to 398)
Tsuchiya,T., Ando,A., Ogawa,C., Futagami,K., Watase,T. and Kowyama
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Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
Unpublished
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/organism="cc..."
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/note="Differentially expressed cDNA library of optic tectum of pigeon with removal of left retina"
/note="Differentially expressed cDNA library of optic tectum of pigeon with removal of left retina"
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Library constructed by N. Garrett, K. Ryan and A.M. Zorn,
(Wellcome/CRC Institute). DNA Sequencing by: Washington University
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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llarity 100.0%; Pred. No. 4.5e-136;
Conservative 0; Mismatches 0;
Shanghai Tiedao University Medical School
Gonghexin Kd.1238, Shanghai, 20070, China
Email: jinroxia@public.sta.net.cn.
Location/Qualifiers
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Xenopus laevis
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BI941233.1 GI:16255705
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                                                               Email: est@watson.wustl.edu
Library constructed by N. Garrett, E. ellefroid, and A.M. Zorn
(Wellcome/CAC Institute). DNA Sequencing by: Washington University
Genome Sequencing Center.

Clone distribution: Xenopus clones from this library are available
trrough the T.M.A.O.E. Consortium/LINIA at: info@image.llnl.gov
Seq primer: -40RP from Gloco
High quality sequence stop: 291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF361564 1inear EST 24-NOV-2000 pot-1-64 Differentially expressed cDNA library of optic tectum of pigeon with removal of left retina Columba livia cDNA, mRNA
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/lab host="DH10B (phage-resistant)"
/clone_lib="wellcome GRC pRN3 St19 26 egg animal cap"
/note="Vector: pBSRN3; Site 1: Not1; Site 2: EcoR1; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
102 c 109 g 102 t
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Lu, Lu, Xu, Lu, Yang, C, Li, X. and Wang, Y.
A profile of differentially expressed genes in P10 pigeon optic tecta with removal of left retina after posthatching first day by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4785984"
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Columba livia
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Department of Biochemistry
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Matches 290; Conservative
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                                                                                                                                                                       /organism="Xenopus laevis"

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/do_type="mRNA"

/do_type="mRNA"

/do_type="msn:8355"

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/clone lib="wellone CRC pRN3 head"

/clone lib="wellone" CRC pRN3 head"

/clone lib="wellone" CRC pRN3 head"

/clone lib="wellone" CRC pRN4 primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library was constructed by N. Garrett, K. Ryan and A.M. Zorn, (Wellcome/CRC Institute). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vigna unguiculata (cowpea)
Vigna unguiculata
Vigna unguiculata
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Sukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
surosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Vigna.
1 (bases 1 to 420)
Denny, R., Danesh, D., Mudge, J., Cooper, A., Larson, K., Fatokun, C. and RFLP sequences of cowpea, Vigna unguiculata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ254218 GQUENCES OF COMPEA, Unionar GSS 21-JUN-2000 cg0029F RFLP sequences of compea, Vigna unguiculata Vigna unguiculata genomic, genomic survey sequence.
AZ254218 GI:8602455
                         available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA 128
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Department of Plant Pathology
University of Minnesota
University of Minnesota
195 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
Tel: 612 625 2225
Fax: 612 625 9728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 Artaardaarcdgccaacgcccaacgcccaacgcccrrr
Genome Sequencing Center Conter Content this library are avail clone distribution: Kenopus clones from this library are avail through the I.M.A.G.E. Consortium/LLNL at: infooimage.llnl.gov Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 336.

High quality sequence stop: 336.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 290; DB 12; I Pred. No. 4.5e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139.0%; Score 290; DB ilarity 100.0%; Pred. No. 4.5c Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                113 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 (
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                                                                                                                                    FEATURES
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Sequence of mapped RFLP marker cg0029 on linkage group vi of cowpea. For more information, see Beandenes at: http://ars-genome.cornell.edu/cgu-bin/MebAcc/webace?db=beangenes&class=Locus. Please see as authorities for mapping/naming: Fatokun, C.A., Danesh, D., Young, N.D. (1993) RFLP linkage map for cowpea (vigna unguiculata (L.) Walp.) in: Genetic Maps, 1992. S. J O'Brien, ed. Cold Spring Harbor Press, Cold Spring Harbor, NY, pp. 6.256-6.258 - and - Menancio-Hautea, D., Xumar, L., Danesh, D., Young, N.D. (1993) RFLP linkage map for munghean (vigna radiata (L.) Wilczek) in: Genetic Maps, 1992. S. J O'Brien, ed. Cold Spring Harbor, NY, pp. 6.259-6.260.
Insert Length: 400 Std Stror: 0.00 Seq primer: M13F Class: RFLP probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Vigna unguiculata"
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//db xref="taxon:1917"
//isue_type="Hypocotyl and roots"
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//dow_stage="Sprouts"
//dome="Yector: pUC 18; Site 1: Pst I; DNA was digested with Pst I: size separated by sucrose gradient centrifugation and the fraction between 500-3000 base pairs ligated into the vector using standard method."
98 a 104 c 112 g 90 t 16 others
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1 'Dases 1 to 424)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
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29.0%; Score 290; DB 28; L
Best Local Similarity 100.0%; Pred. No. 4.5e-136;
Matches 290; Conservative 0; Mismatches 0;
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/mol_type="mRNA"

/db_txef="txon:8355"

/dlone="txef="txon:8355"

/clone="type="dorsal lip"

/lab_host="DH10B (phage-resistant)"

/lab_host="Wellcome CRC pRN3 dorsal lip"

/clone_lib="wellcome CRC pRN3 dorsal lip"

/clone_lib="wellcome CRC pRN3 dorsal lip"

/clone_loot: pBsRN3; Site_1: Not1; Site_2: EcoRI; cDNAs

/were oligo-dT primed and directionally cloned. Staging

according to Nieuwkoop and Faber. Library was constructed

by A.M. Zorn (Wellcome/CRC Institute). "

1 a 106 c 112 g 105 t
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, S., Gibbons, M., Harvey, N., Ritter, B., Jackson, Y., McCann, R., Waterston, R. and Wilson, R., Washu, Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                   Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.B. Consortium/LINL at: info@image.llnl.gov Bossible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTAATCATGGTCATAGCTGTTTCCTGTGTGAATTGTTATCCGCTCACAATTCCACACA 128
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de33f05.x1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone IMAGE:3473792 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                              Unpublished
Contact: Sandy Clifton, Ph.D.
WashU Kenopus EST project, 1999;
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. L.
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Xenopus laevis
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Location/Qualifiers
1. .424
                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Best Local Similarity 100.
Matches 290; Conservative
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BI938097
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| /organism="Kanopus laevis"
| /mol_type="Raxon:8355"
| /mol_type="Raxon:8355"
| /db_xref="taxon:8355"
| /clone="InMARE:3488076"
| /tissue_type="dorsal lip"
| /tissue_type="dorsal lip"
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| /clone="lip" /clone lip="wellcome CRC pRN3 dorsal lip"
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                                                                                                                                                                                                                                                                                                             Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Renopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: 40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 18-OCT-2001
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Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                   USA
                                                                                         Contact: Sandy Clifton, Ph.D.
Washugton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 1
Tel: 314 286 1800
Fax: 314 286 1810
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High quality sequence stop: 397.
Location/Qualifiers
      Waterston, R. and Wilson, R.
WashU Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                  Email: est@watson.wistl.edu
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                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.B. Consortium/LiNL at: info@image.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 379.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

1. (bases 1 to 424)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.; Person, R., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Watcherton, R. and Wilson, R., Washu Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3473792"
/tissue_type="dorsal lip"
/lab_nost="DHIOB (phage-resistant)"
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Fax: 314 286 1810
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                                                                                                                                                      Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
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/organism="Xenopus laevis"
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/db_xref="taxon:8355"
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Email: est@watson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 309.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="dorsal lip"
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                                                                                                                                                               Person
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                                                      Euteleostomi;
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de35h10.xl Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clon«
IMAGE:3473922 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN. ;,
mRNA sequence.
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                                                                           Xenopodinae; Xenopus.
1 (bases 1 to 424)
1 (bases 1 to 424)
Clifton, S. Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pa Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., P., B., Gibons, M., Harvey, M., Ritter, E., Jackson, Y., McCann, R., WashU Xenopus EST project, 1999
Unpublished
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                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 4.5e-136;
Xenopus laevis (African clawed frog)
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|db_xref="taxon:8355"
|clone="IMAGB:3473876"
                            Kenopus laevis
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                        Contact: Sandy Clifton, Ph.D.
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de41b11.x1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone IMAGE:3474380 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN: ;,
                                                                                                                                                                                                                                                                                                                                                       Contact: Sandy Clifton, Ph.D.
WashU Xenogus EST project, 1999
WashU Xenogus EST project, 1999
444 Forest Park Parkway, Box 8501, St. L
11 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                      Xenopus laevis (African clawed frog)
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Location/Qualifiers
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Matches 290; Conservative
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(Lipasea 1 to 424)

(Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person War, Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Wash, Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: estewatson.wustl.edu
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Center
Sequencing by: Washington University Center
Clone distribution: Kenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 375.
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="Wellcome CRC phy3 dorsal lip"
/note="Vector: pbsRN3; Site 1: Not1; Site 2: EcoR1; cDNAs were cligo-dT primed and directionally cloned. Staging were cligo-dT primed and directionally cloned. Staging were constituted by A.M. Zorn (Wellcome/CRC Institute). "
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Contract: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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100.0%; Pred. No. 4.5e-136;
Live 0; Mismatches 0;
                                                               Xenopus laevis (African clawed frog)
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/mol_type="mRNA"
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        BI938185
BI938185.1 GI:16252657
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/un_Arsi-temporal 1ip"
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a 106 c 112 g 105 t lothers
                                                                    Xenopodinae; Xenopus.

(bases 1 to 424)

(lifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Washu Xenopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov Possible reversed clone: similarity on wrong strand seq primer: -40UP from Gibco
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Xenopus laevis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 CGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACA
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Pred. No. 4.5e-136;
0; Mismatches 0;
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106 c 113 g 106 t
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Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Library can available
Clone distribution: Kanpus clones from this library are available
through the I.M.A.G.E. Consortium/Libr at; info@image.llnl.gov
Fossible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 397.
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Neuraryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases I to 424)

1 (fases I to 424)

Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person, Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person, Waterston,R. and Wilson,R.

WashU Xenopus EST project, 1999
                                                   BI938341 424 bp mRNA linear EST 18-OCT-2001 de41f04.x1 Wellcome CRC pRN3 dorsal lip Xenopus laevis cDNA clone IMAGE:3474558 3' similar to TR:Q44068 Q44068 ALPHA-HEMOLYSIN. ;,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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29.0%; Score 290; DB 12; Length 424;
Best Local Similarity 100.0%; Pred. No. 4.5e-136;
Matches 290; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
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                                                                                                                                                                                              BI938341.1 GI:16252813
                                                                                                                                     mRNA sequence.
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309 CCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCGGTA 358
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Search completed: February 16, 2004, 03:15:45 Job time : 2640.53 secs

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February 15, 2004, 19:10:26; Search time 3961.99 Seconds (without alignments) 10335.846 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Pred.

1300 bp DNA linear BCT 02-SEP-1999 encoding neomycin and kanamycin resistance the reading frame of a further protein. 101012 Sequence 4 E02455 DNA encodin AR067785 Sequence M84115 Cloning vec AY048743 Template
A00782 Plasmid pDM
A02297 Plasmid pDM
A02297 Plasmid pDM
A07054 Artificial
A10362 Artificial
A14595 Synthetia
A14595 Synthetia
A14595 Synthetial
A30452 plasmid pDM
AR096518 Sequence
AR098395 Sequence
AR098395 Sequence
AR098395 Sequence
AR07786 Sequence
AR12638 Sequence
AR218546 Sequence
AR218545 Sequence
AR218545 Sequence
AR218545 Sequence Mammary c Antimicro Transposon ThS fragment encoding neomycin and kanamycin resistance (neo) and a fragment of the reading frame of a further protein. V0618 J01834
V0618 J01834
V06618.1 GI:43748
drug resistance gene; neomycin resistance; transferase.
Bscherichia coli
Bscherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriace, Escherichia.
I (bases I to 1300)
Beck, E., Ludwig, G., Auerswald, E.A., Reiss, B. and Schaller, H. Nucleotide sequence and exact localization of the neomycin Polynucle Apoptosis Vascular AR134671 Sequence AR219195 Sequence A9266 Sequence 2 AR137192 Sequence AR158346 Sequence AR241208 Sequence Apoptosis Sequence Sequence Sequence BD005772 Therapeut AR207828 Sequence U32991 Escherichia Therapeut V00618 Transposon Sequence Sequence Sequence Seguence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AR267137 & BD022735 b BD022735 b BD129548 E BD131214 b BD134899 BD134899 BD136632 T AR134670 E AR219194 S AX589681 S AR134669 S AR219193 AR266415 ALIGNMENTS SUMMARIES ISTN5X 101012 B02455 AR067785 SYNKANRA BCU32991 AY048743 AR218546 AR253199 AR266379 AR09839 A14595 A19608 DB Length 2020 33974 33974 33974 4798 4797 3974 3974 3974 33974 33974 33974 33974 3984 Query Match 1 100.0 100.0 100.0 100.0 ISTNSX Score ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE RESULT 1 ISTN5X/c LOCUS Result No. υ υ

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780 305 840 245 960

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PAT 21-MAY-1993
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                                              GCCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT
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                      GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATACTT
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Unclassified.

1 (bases 1 to 1300)

3 Puhler, A., Rellaender, H. and Weber, G.
Nitrogen fixation regulator genes
L. Patent: US 4782022.A 401-NOV-1988;
Lubrizol Genetics, Inc., Wickliffe, OH
Location/Qualifiers
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/bx xetf="GI:43749"

/db xref="SWISS PROT:P00552"

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/note="unidentified reading frame"
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904 241 844 301 784 361	724 AGGCATCGCCATGGGTCACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG 421 CGAACAGTTCGGCTGGCGGGGGCGAGCCCTGATGCTCCTCCAGATCATCCTGATCGAAA [000 001 002 003	661 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG 72 1 1 1 1 1 1 1 1 1	Oy 721 TGGCCAGCACGATAGCCGCGGTGCCTCGTCCTGCAGTTCATTCA	OY 781 CGGTCTTGACAAAAGAACGGCGCCCTGCGCTGACGCCGGAACACGGCGGCATCAG 840	Oy 841 AGCAGCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG 900	Qy 901 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTTT 960	OY 961 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001	RESULT 3 E02455/c LOCUS LOCUS DEFINITION DA encoding aminoglycoside 3'-phocphotransferasell(APH). ACCESION B02455.1 G1:2170686	KEYWORDS JP 1990150282-A/1. SOURCE Transposon Th5 ORGANISM Transposon Th5 transposons.	REFERENCE I (bases I to 1600) AUTHORS Yoshida,N., Kikuchi,N., Shin,M. and Teraoka,H. TITLE MODIFIED HUMAN PSTI JOURNAL PETENT: UP 1990150282-A 1 08-JUN-1990;	COMMENT STANDOR TIP COMMENT OS TRANSPOSON TIP PN JP 1990150282-A/1

Oy 361 AGGCATCGCCATGGGTCACGACGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG 420 1292 AGGCATCGCCATGGGTCACGACGACTCTCGCCGTCGGGCATGCGCCTTGAGCCTGG 1351	Qy 541 GGCAGGTAGCCGGATCAAGCGTATGCATTGCATCAGCCATGATGGATG	61 GCCAGTCCTTCCGCTTCAGTGACAACGTCGAGCAGCTGCGCAAGGAACGCCCGTCG 7		SYNKANRA LOCUS LOCUS LOCUS CLONING Vector PHSS6 kanamycin resistance protein (neo) gene, putative cds. ACCESSION VERSION W84115.1 R84115.1 RAMAMYCIN resistance protein (neo) gene, M84115.1 KEYWORDS SOURCE ONGANISM Unidentified cloning vector artificial sequences; vectors. AUTHORS LISITE AUTHORS Selfert, H.S., So,M. and Heffron,F. TILLE LITLE LITLE LITLE LITLE AUTHORS Selfert, H.S., Chen,E.Y., So,M. and Heffron,F. TITLE CLOSEFERICE Selfert, H.S., Chen,E.Y., So,M. and Heffron,F. AUTHORS Selfert, H.S., Chen,E.Y., So,M. and Heffron,F. AUTHORS Selfert, H.S., Chen,E.Y., So,M. and Heffron,F. Shuttle mutagenesis: a method of transposons into transformable organisms JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for Saccharomyces cerevisiae JOURNAL Shuttle mutagenesis: a method of transposon mutagenesis for JOURNAL Shuttle mutagenesis: a method of transposon mutagen
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Microbiology and Immunology, University of Adelaide, Frome Road,
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Pinyon, R.A. and Thomas, C.J.
DNA sequence of a mini-Tn5 transposon (mini-Tn5 Km)
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Bscherichia coli mini-Tn5 kanamycin transposon.
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91035272
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                                                                                                                                                                                                                /note="M13 origin in derivative pHSS7; single stranded DNA replication origin; a 191 bp fragment from pS11 (Johnston & Ray, JMB 177:685-700, 1984) was inserted at this position to make the derivative pHSS7"
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1001; DB 12; Length 2320;
                                                                                                                                              /note="putative cds; putative"
/function="kanamycin restistance gene from In5"
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
            'organism="unidentified cloning vector"
                               /mol_type="genomic DNA"
/sub_species="Cloning vector pHSS6"
/db_xref="taxon:45196"
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                                                                                                                                                                                                                                                                                                                       /note="putative"
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de Lorenco,V. Herrero,M., Jakubzik,U. and Timmis,K.N.
Mini-Ths transposon derivatives for insertion mutagenesis, promoter probing, and chromosomal insertion of cloned DNA in gram-negative
                                                                                                                                                                                                                                                                                                                                                                                           995 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG 1054
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780
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Gene 29 (3), 303-313 (1984)
                                                                                                                                                        781 CGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGCGGGGGCATCAG
875 redecadecacearadecedecerecreerecreereraticarreaceacacedearacer
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J. Bacteriol. 172 (11), 6557-6567 (1990)
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organism="Template plasmid pKD4"
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/note="natural FRT site"
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/db_xref="taxon:170492"
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Template plasmid pXD4
artificial sequences; vectors.
1 (bases 1 to 3267)
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Datsenko, K.A. and Wanner, B.L.
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/product="neomycin phosphotransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                     LSSHLAPAEKVSIMADÄMRRLHTLDPÄTCPFDHQAKRRIERARTRNBAGLVDQDDLDE
EHQGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGPIDCGRLGVADRY
QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
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               On Jan 23, 1996 this sequence version replaced gi:1000122.
Location/Qualifiers
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/note="Tn5 O end functional in transposition"
/citation=[4]
                                                                                                                                                                                         note="Tn5 I end functional in transposition"

    1651
    function="neomycin and kanamycin resistance"

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                                                                /organism="Escherichia coli"
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/strain="SMIO (lambda pir)"
/db_xref="taxon:562"
/plasmid="mini-Tn5 Km"
/transposon="mini-Tn5 Km"
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Adelaide, S.A. 5001, Australia
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Datsenko, K.A. and Wanner, B.L. One-step inactivation of chromosomal genes in Escherichia coli K-12
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                                    1250 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCGCTTGCATTGCATCAGCCATGATGGATACTT 1191
                                                                                                                                                                                               1190 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCGGCACTTCGCCCAATAGCA 1131
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                                                                                                                                  TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA 660
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541 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT 600
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Submitted (29-UUL-2001) Biological Sciences, Purdue University,
Lilly Hall of Life Sciences, West Lafayette, IN 47907, USA
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6640-6645 (2000)
20300954
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/db_xref="G1:15554333"
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PAT 16-FEB-1993
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                                                                                                                                                                                                                     121 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT 180
   912 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG 853
                                                                                                                                                                                                                                                                                                                                                         732 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAAACGCCCGTCG 673
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                                                                GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT
                                                                                                                    852 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCATTGCATCAGCCATGATGGATACTT
                                                                                                                                                                                 601 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA
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Patent: BP 0309746-A 11 05-APR-1989;
F. HOFFMANN-LA ROCHE AG
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KEYWORDS
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SSHLAPAREKYSIMDAMKHHILDFATCPPPJQAKRI EEKATRWEAGLVDQDDLDE
EHGGLAPAELFARIKARMPGEDLVYTHGDACLPNIKVENGRESGFIDGRLGVADRY
QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDBFF"
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YSPVTEKHLIDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
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/translation="MSIQHFRVALIPPFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
/translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR
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/note="bla; ampicillin resistance"
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/note="common priming site kl"
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FEATURES Location/Qualifiers 13740 /organism="synthetic construct" /mol_type="genomic DNa" /db_xref="taxon:32630" BASE COUNT 813 a 1035 c 1056 g 836 t	Query Match 100.0%; Score 1001; DB 6; Length 3740; Best Local Similarity 100.0%; Pred. No. 0; Matches 1001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		61 AAGGCGGCGGTGGAATCCAAATCTCGTGATGGCAGGTTGGCGCTTGGCTTGGTCGGTC	121 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAGGCGTTGCGCTTTGTTTTTTTT	181 GCGAATCGGGAGCGCGGTACCGTAAAGCACGAGGAAGCGGTCAGCCATTCGCCGCCAA 		QY 301 GCGGGCCACAGTCGATGAATCCAGAAAAGGGGCCATTTCCACCATGATATTCGGCAAGC 360	Oy 361 AGGCATGGGCATGGGTCACGAGATCCTCGCCGTCGGGCATGCGCGCTTGAGCCTGG 420	Oy 421 CGAACAGTTGGGCGGGGGGCGCTGATGCTCTTGGTCCAGATCATGGACAA 480	Qy 481 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGTGTTTCGCTTGGTGGTCGAATG 540 DD 810 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCTTTTCGCTTGGTGGTCGAATG 751	OY 541 GGCAGGTAGCGGATCAAGGGTATGCAGCGGCATGCATCAGCCATGATACTT 600 Db 750 GGCAGGTAGCCGGATCAAGCGTATGCAGCGCGCATTGCATCAGCCATGATGGATACTT 691	Oy 601 ICTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA 660	Qy 661 GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAACGCTGCGCAAGGAACGCCCGTCG 720 Db 630 GCCAGTCCCTTCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG 571	0y 721 TGGCCACCACGATAGCCGCGCTCCTCCTCCTGCAGTTCATTCA	Oy 781 CGGTCTTGACAAAAAGAACCGGGGCGCCCTGCGCTGACAGCGGAACACGGGGGGGTTCAG 840	QY 841 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG 900 L	Qy 901 GAGAACCTGCGTGCAATCCATCTTGTTCAATCGAAACGAACCTCATCCTGTCTTT 960
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Db 750 GGCAGGTAGCCGGATCAAGCGTATGCATCACCATCACCATGATGCA 60	RESULT 11 A07054/c LOCUS LOCUS LOCUS LOCUS LOCUS A07054/c A07054/c A07054/c A07054/c A070551/c Surtheric construct COURGANISM Surtheric construct COURGANISM Surtheric construct COURGANISM Surtheric construct COURGANISM Surtheric construct COURGANISM Surtheric CONSTRUCT CONSTRUCT COURGANISM Surtheric CONSTRUCT CONSTRUCT COURGANISM Surtheric CONSTRUCT CONSTRUCT CONSTRUCT COURGANISM Surtheric CONSTRUCT CONSTRUCT COURGANISM Surtheric CONSTRUCT CONSTRUCT CONSTRUCT COURGANISM Surtheric CONSTRUCT CO
DD 390 GAGAACCTGCTATCATCTATCATCATCTTCTTTTTTTTTT	Delight State 100.04; Score 1001, DB 6; Length 3740; Delight Match 100.04; Score 1001, DB 6; Length 3740; Delight State 100.04; Pred. No. 0; Matches 1001; Conservative 0, Mismatches 0; Indels 0; Gaps 0; 1290 CGCTGGAGGATCATCAGCGGGGGTGCCGGAAACGATTCGAAGCCCTACCTTCATAG 0 120 GGCTGGAGATCATCAGCGGGGGTGCCGGAAACGATTCGGAGGCGAACCTTTCATAG 1231 Delight MAGGGGGGGGGAATCGAAATCTCGTGAATGGCAGTTGGAGGTGATT 1101 Delight MAGGGGGGGGGAATCGAAATCTCGTGAATGGCGAGTTGGTCGATTT 1101 Delight MAGGGGGGGGGAATCGAAATCTCGTGAAGGCGATTGGTCGATTT 1101 Delight MAGGGGGGGGGAATCGAAAATCTCGTGAAGGCGATTGGTCGATTT 1101 Delight MAGGGGGGGGGAATCCGAAAAACTCGTCAAGAGGCGATTGGTCGCATT 1101 Delight MAGGGGGGGGAATCCGGAAAACTCGTCAAGAGGCGATTGGTCGCATT 1101 Delight MAGGGGGGGGAATCCGGAAACTCGTCAAGAGGCGATTGGTCGCCATTGGTCGCCATT 1101 Delight MAGGGGGGGGAATCCGTAAACTCGTCAAGAGGCGATTGGTCGCCATTGGTCGCCATTGGTCGCCCATTGGTCGCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCCATTGGTCGCCATTGGTCGCCCCATTGGTCCCCCATTGGTCCCCCCATTGGTCCCCCCATTGGTCCCCCATTGGTCCCCTCTGATGGTCTTCGTCCCATTGGTCCCTCTGATGGTCTCTGTCCATTGGTCCTTGATGTCTTCGTCCCATTGGTCCTGTCGATGGTCCTGTTGGTCCTGTTGGTCCTGTTGGTCCTGTTGGTCGTC

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Bujard,H. and Lanzer,M.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
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M synthetic construct

artificial sequences

1 (bases 1 to 3740)

Bannwarth, W. (Sapers, P., Le Grice, S. and M Recombinant HIV-2 polypeptides

Patent: EP 0316695-A 6 24-MAY-1989;

F. HOFFWANN-LA ROCHE AG

1. 3740

| 1. 3740|
| / Organism="synthetic construct"
| / mol_type="genomic DNA"
| / db_xref="taxon:32630"
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/product="lac repressor"
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FSHEDGTRLGYTEHLVALGADVGGLIINYPLDAGBLSSVSARLRLAGGHKYLTRNQIQPIAEREG
DWSANGSGFQOTHOMINGSTIVOTALVANDQMALGANRAITESGLRVGADDT
GDSSCYT PPLITIKOPPRILGQTSVDRLQLSQGGAVKGNQLLPVSLVKRKTTLABNT
GTASFRALADSIMQLARQVSRLESGG"
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1 (bases 1 to 3740)

Bannwarth, W., Certa, U., Mous, J. and Stueber, D.
Polypeptides that elicit antibodies against AIDS virus
Polypetent: BP 0219106-A 8 22-APR-1987,
F. HOFFMANN-LA ROCHE AG

Location/Qualifiers
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Soluble interferon-gamma receptors and methods for their patent: sp 0393502-A 16 24-0CT-1990;
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Search completed: February 16, 2004, 01:25:58 Job time : 3968.99 secs PHEA-5 expression Vector pHE4-5. Ch Nucleotide sequenc PHE4-5 vector, con Vector plasmid pHE PAPAI pHE4-5 expre Expression vector Nucleotide sequenc Expression vector Expression vector PHEA vector nucle PHEA expression

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Chimeric - Bos taurus.
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pDMI.1 contg. the
Sequence of plasmi
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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- 2004 Compugen Ltd.
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Tn5 transposase gene; E. coli; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of novel vector plasmid pUNI-10. It includes: the conditional origin of replication from R6K-gamma, derived from plasmid R6K (ATCC 3720); a Not1-Kpn1 polylinker that derilitates the exchange of lox sites; a wild-type loxP site (see also AAZ58066); a polylinker used for the insertion of genomic DNA or CDNA sequences; a bovine growth hormone polyA site; a T7 terminator; and a kanamycin remissed for the insertion of genomic DNA or cample of novel Univertors or pUNI vectors of the invention is an example of novel Univertors or pUNI vectors of the invention is an example of novel Univertors or pUNI vectors of the invention is an example of novel Univertors or pUNI vectors of the invention is that have a sequence-specific recombinase target site (e.g. loxP) preceding the insertion site for the gene of interest, a selectable marker gene (optional) and a conditional origin of replication factor (optional). The vectors are designed to contain a active only in host cells expressing the requisite transacting replication factor (optional). The vectors are designed to contain a gene of interest but to lack a prometer for expression of the subcloming of mucleic acid sequences. The method is referred to subcloming of mucleic acid sequences. The method is referred to subcloming of mucleic acid sequences in vivo and in vitro without the need of restriction endomucleases. The method is referred to set the need of restriction endomucleases. The method is referred to sea the Univector Plasmid fusion events are under the control of novel regulatory elements. A second UPS-related method allows for the precise transfer of coding sequences alone from cubic model weet the control to a host vector. UPS further provides means for the subcloning of entire nucleic acid libraries and the directional
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/note= "kanamycin resistance gene from Tn5"
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                       /*tag= e
/note= "BGH polyA site"
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Matches 1001; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence shown is that of a novel transposon useful for sequencing long DNA sequences. The transposon comprises a partial sequencing long DNA sequences. The transposon comprises a partial phages SPG and T7 inserted near the opposite ends of Tn5. At each terminus a segment of 19 nucleotides of either the O-end or I-end of Tn5 are present and restriction enzyme sites are positioned throughout the sequence (sep. with one at either end, less than 20 bases from each terminal segments of Segments of foreign DNA of at least 17 bases are positioned directly adjacent to each restriction site. The transposon also comprises a Tn5 transposate gene insert and a kanamycin selectable marker for the transposable DNA unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGCTGGAGGATCATCCAGCCGCCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1340 CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAACGATTCCGAAGCCCAACCTTTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1220 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOGAATOGGGAGGGGGGATACCGTAAAGCACGAGGAGAAGCGGTCAGCCCATTCGCCGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1160 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGGCCACAGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1040 GCCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1001; DB 14; Length 3176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bidirectional sequencing of long DNA molecules - by inserting transposon Tn5seq1 into DNA molecule of E coli cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3176 BP; 661 A; 898 C; 893 G; 724 T; 0 other;
                                                                                                                                      /*tag= z
/note= "O-end of Tn5 transposon"
                                                                            /*tag= y
/note= "BamHI site"
3158..3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 4; 17pp; English.
                        '*tag= x
'note= "SP6 .RNA"
1142..3147
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                                                                                                                                                                                                                                                                                                       87US-0105422
90US-0508379
    3042..3157
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                                                          misc_feature
                                                                                                                  misc_feature
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12-APR-1990;
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misc_RNA
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                                                                                                                                                                                                                                                                                                                     *tag= e
note= "codes for kanamycin selectable marker"
                                                                                                            transposon sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= n
note= "tnp (Tn5 transposase gene)"
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note= "Eco47III restriction site"
                                                                                                                                                                                                                                                                                                                                                   /*tag= f
//tag= f
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//note= "SphI restriction site"
//tag= h
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note= "HindIII restriction site"
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note= "BamHI restriction site"
76..381
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tag= j
hote= "Asull restriction site"
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note= "SacII restriction site"
856..2861
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10te= "AvaII restriction site
                                                                                                                                                                                                                                                             *tag= d
note= "Bcll restriction site'
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note= "NruI restriction site"
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note= "SalI restriction site"
omplement (1549..2979)
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*tag= p
note= "NheI restriction site"
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note= "XhoI restriction site"
511..2617
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note= "SapI restriction site"
881..2886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= w
note= "Hpal restriction site"
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note= "NotI restriction site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'tag= q
hote= "BsmI restriction site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= k
note= "SmaI restiction site"
                                                                                /*tag= a
/note= "O-end Tn5 t:
complement (1..29)
                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the Thisegal transposon used in the method of the invention. The method is for RNA transcription, and comprises the insertion of the Thisegal transposon into an E. coli DNA molecule to obtain hyperexpression of genes adjacent to strong promoters SP6 or T7. The transposon is useful for stimulating the transcription of genes adjacent to the heterologous SP6 or T7 promoters in E. coli, for making RNA transcripts in vitro and the hyperexpression or specific transcription of genes (adjacent to the SP6 or T7 promoters in I. vivo. This sequencial as a less laborious method of sequencing long DNA molecules than current methods such as base-specific chemical cleavage and enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     981
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100.0%; Score 1001; DB 20; Length 3176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                            Obtaining hyperexpression of genes in Escherichia coli hosts insertion of transposon Tn5seq1 such that the strong SP6 and promoters are adjacent to the host genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3176 BP; 661 A; 898 C; 893 G; 724 T; 0 other;
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                                                                                                                87US-0105422.
90US-0508382.
93US-0004406.
                                                                                                                                                                                                                                                                                        DK;
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                                                                                                                                                                                                                                WASHINGTON
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                                                                                                                                                                                                                                                                                                                                          WPI; 1999-152772/13
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                                                                                                                05-OCT-1987;
12-APR-1990;
14-JAN-1993;
                                                                                                                                                                                                                             VINU ( WINU)
                                                             14-JAN-1993;
        09-FEB-1999
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                                                                                                                                                                                                                                                                                     Berg DE,
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strong promoter; SP6 promoter; T7 promoter; ss.
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                                                                                                                                                                                                                                                                                                                           Transposon Insseq1 was constructed from the pBR322-derived plasmid pBR322.46rrived plasmid pBR322.40rrived bransposon is contained in plasmid pBRG1408. Ican be used for sequencing bacterial genomic DNA without recombinant DNA cloning and also for sequencing DNA cloned in phages or multicopy plasmids. It may also be useful for RNA sequencing with SP6 and IT RNA polymerases, for making RNA transcripts in vitro and for hyperexpression or specific transcription of adjacent genes in
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screening of DNA sequences
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Phage T7; RNA polymerase; DNA sequencing; ss.
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AAQ27504 standard; DNA; 3177
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                                                                                 Plasmid encodes a fusion protein consisting of 1 or 2 affinity peptides bonded directly or indirectly to a biologically active protein (i.e. dibydrofolate reductase). The presence of adjacent His residues in the affinity peptides allows purificn of the biologically active protein by see also AAR80955-8 and AAN80960-63. (Updated on 25-WAR-2003 to correct PR field.)
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100.0%; Score 1001; DB 9; Length 3740;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                           Sequence 3740 BP; 813 A; 1035 C; 1056 G; 836 T; 0 other;
                                     pp; German
                                        Disclosure, Page ?;
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                                                                                      CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCCAACCTTTCATAG
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AAN81154 standard; DNA; 3740 BP.
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Matches 1001; Conservative
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                                                                                                               1050 GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCCCCACACCA
181 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
                                                                                    GCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCA
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                                                    HTLV-III; env protein; gag protein; AIDS; immunogenic activity;
vaccines: dlagnosis; oligonucleotides; pDMI.1; neo-gene; lacl-gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1170 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
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E.Coli transfected with pDS5/RBSII,33+5A (AAN80481), pDS8/RBSII (AAN80482) or derivatives, cantg. a HTLV-gene, also contain plasmid pDMII. Expression is possible by addition of IPTG to the medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide with immunogenic activity of HTLV 3 env-gag protein - useful in vaccines and for AIDS diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lacl-gene: P.J. Farabaugh, Nature 274, 765-769 (1978) contg. the mutation Iq (M.P. Calos, Nature 274, pp. 762-765 (1978) for the lac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene is added.

The DNA encodes peptides useful as active ingredients in vaccines and for detecting AIDS antibodies in serum etc.

See also AAN80480-85.

(Updated on 25-WAR-2003 to correct PD field.)

(Updated on 25-WAR-2003 to correct PR field.)

(Updated on 25-WAR-2003 to correct PR field.)

(Updated on 25-WAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1001; DB 9; Length 3740;
.larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0;
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kanamycin resistance of E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3740 BP; 813 A; 1040 C; 1051 G; 836 T; 0 other;
             contg. the neo-gene of Tn5 and the lacl-gene.
                                                                                                                                                                                                           *tag= a
product=neomycinphosphotransferase
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/*tag= b
/product=lac-repressor
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                                                                                                                                                               Location/Qualifiers
357..1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mous J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86GB-0029116
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Best Local Simi;
Matches 1001; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-1986;
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                                                                                                                                                                                                                                                                                                                                      EP270114-A.
                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repressor.
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    GACCGGCTTCCATCCGAGTACGTGCTCGATGCGATGTTTTCGCTTGGTGGATG
                                                                 GCCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCATGATGGATACTT
                                                                                                                   TCTCGGCAGGAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA
                                                                                                   TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCA
                                                                                                                                                        GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCG
                                                                                                                                                                            GCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACCAGCTGCGCAAGGAACGCCCGTCG
                                             GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATACTT
                                                                                                                                                                                                                             781 CGGTCTTGACAAAAGAACCGGCGCCCCTGCGCTGACAGCCGGAACACGCGGCATCAG
                                                                                                                                                                                                                                                                                                                        A 1.2 kb insert from lambda 5-7 was isolated, ends were repaired with Klenow polymerase and BamHI linkers were ligated to both ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 GAICAGAICTIGAICCCCTGCGCCATCAGAICCTIGGCGGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merozoite; antigen; vaccine; coccidiosis; RBS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen (23kD), D
in the prodn. of
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AAQ12786 standard; DNA; 3740
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(first entry)
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recombinant virus, useful
coccidiosis in poultry
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09-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                     IFN-gamma is a therapeutically active agent in the treatment of autoimmune disease, allograft transplant rejections, multiple sclerosis, chronic inflammations and delayed hypersensitivity. It also useful in identifying IFN-gamma agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 1001; DB 11; Length 3740;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                         treating auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3740 BP; 813 A; 1035 C; 1056 G; 836 T; 0 other;
                          /*tag= a
/label= Neomycin phosphotransferase.
complement(1531..2609)
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                   Soluble interferon-gamma receptors - for diseases, chronic inflammations, etc.
                                                                 /*tag= b
/label= lac repressor
                                                                                                                                                                                                                                                 Stuber D;
Location/Qualifiers
357..1146
                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 16; 174pp; English.
                                                                                                                                                                                                                   (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                Garotta G,
                                                                                                                                                                 90EP-0106992
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                                                                                                                                                                                                                                             Fountoulakis M,
                                                                                                                                                                                          11-APR-1990;
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Key
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This sequence represents the plasmid pDMI.1. This plasmid was used in conjunction with the expression plasmids pDS56/RBSII, -1, and -2. These plasmids contain the regulatable promoter/porator element (N250FSNI50F29 and the ribosomal binding sites (RBS) RBSII, RBSII(-1) and RBSII(-2) respectively. These RBS are derived from the RBS of the promoter pg25 of the B. coli phage TS. These plasmids may be maintained in E. coli play if the promoter/operator element is repressor is encoded by the lacingenessor to the operator. The lac repressor is encoded by the lacingenessor to the operator. The lac repressor is encoded by the lacingenessor to the operator. The lac repressor is encoded by the lacingenessor to the operator. The lac present in the calls. Therefore the lacing allele, which contains a promoter mutant responsible for increased expression of the repressor contains the neowych phosphotransferase gene from the plasmid pACYC184 which contains all the information required for the plasmid between bases 1-1120 contains the replication and stable transmission to daughter cells. The region of these plasmids between bases 1-1120 contains the replication region and the gene for beta-lactamases gene is mediated by elimination of the Hincill and Petl cleavage sites. These plasmids also contains the enzymes Sall, Petl and Hindill,
                  450 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                   GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTTT
                                                                                    390 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT
                                                                                                                                                                                                                                                                                                                                                                                            Plasmid; pDS56/RBSII; -1; -2; regulatable; promoter; operator; N250PSN250P29; ribosomal binding site; RB5; RB5II; RB5II(-1); RB5II(-1); PQ25; B. coli; phage; T5; lac; repressor; lacI; lacIq; pDMI.1; replication; beta-lactamase; terminator; lambda; CAT; T1; chloramphenicol aceryltransferase; rrnB operon; reading frame; neomycin phosphotransferase; Tn5; transposon; selection marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic specified polypeptide and fragments - capable inducing an immune response against eimeria parasites and from proteins produced by these parasites
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                                                                                                                                          330 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
                                                                                                                    GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
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13-MAY-1993
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                                                                                                                                                                                                                                        Gaps
The modified fragment was inserted into each of pDS56/RBSII, pDS56/RBSII-1, and pDS56/RBSII-2. Plaemids contg. the inserts in both possible orientations were transformed into E. colistrain MIS carrying the compatible pDMI.1. The E. colistrain MIS contg. plasmids pSD56/RBSII and pDMI.1 is described in EP-316695.
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0
                                                                                                                                                                                                       Length 3740;
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                                                                                                                                                                  Sequence 3740 BP; 809 A; 1039 C; 1056 G; 836 T; 0 other;
                                                                                                                                                                                                 DB 12;
                                                                                                                               (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                   100.0%; Score 1001; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                    0; Mismatches
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Best Local Simil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the nucleotide sequence of bacterial expression vector pHE4a. This vector includes a neomycin phosphorransferase gene as a selectable marker, an Escherichia coll origin of replication (oric from pUC129), a phage T5 promoter sequence, 2 lac operators (see also AAV33722), a Shine-Dalgarno sequence, the lactose operon repressor gene (lacig) and a multiple cloning site linker region. Expression of operatively linked sequences located downstream from the lac operators may be induced by addition of a lac operon inducer such as IPTG. pHE4 vectors have been produced that include the coding sequence (see AAV3367) for novel human thymus receptor tyrosine kinase (TRIK, see AAW70525-26). These can be used for the
                                                                                                                                                                                                                                                                                                                                                         Thymus receptor tyrosine kinase; TRTK; LERK; Eph; colon carcinoma; testicular carcinoma; pancreatic carcinoma; lung adenocarcinoma; breast carcinoma; heptacellular carcinoma; cancer; cell proliferation; diagnosis; therapy; prognosis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated thymus receptor tyrosine kinase - is used to develop products for the diagnosis and treatment of cancers and other diseases involving aberrant cell proliferation
                                                                                  GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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                                                                                                          GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
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Chimeric - Bacteriophage T5
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the terminator of E. coli phage lambda, the promoter-free gene of chloramphenicol acetyltransferase (CAT) and the terminator T1 of the E. coli rrnB operon. These plasmids differ by one nucleotide following the ATG start codon resulting in protein expressio in all
                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                Sequence 3740 BP; 813 A; 1035 C; 1056 G; 836 T; 0 other;
                                                                        three potential reading frames. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2579 CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAG
     GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT
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                                                                                                                                                                                                                                                                                                                                                         Cardiac and pancreatic protein; CAPP; muscle-derived growth factor; human; pandreatitis; myocardial infarction; cardiomyopathy; vector; pHE4a; ds.
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e.g. pancreatitis
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100.0%; Pred. No. 0;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cardiac and pancreatic protein
products for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 73-75; 113pp; English.
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Chimeric - bacteriophage T5.
Chimeric - synthetic.
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 production of recombinant TRTK polypeptides in bacterial host cells
                 The invention provides TRTK polynuciectides and polypeptides, vectors, host cells and recombinant methods of producing these. Also provided are diagnostic methods for detecting disease states associated with the aberrant expression of TRTK and therapeutic methods for treating such disease states, especially cancer.
                                                                                                                                                                   100.0%; Score 1001; DB 19; Length 3974; 100.0%; Pred. No. 0;
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                                                                                                                               Seguence 3974 BP; 899 A; 1116 C; 1095 G; 864 T; 0 other;
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ELL2; RNA polymerase II elongation factor; human; neoplastic leukaemia; inhibitor; diagnosis; susceptibility; ds.
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The present sequence represents pHB405 vector which contains human myelin oligodendrocyte glycoprotein-like protein (MOGp). The presence of MOGp on the surface of oligodendrocytes is associated with oligodendrocyte maturation and with the production of myelin. Products from the present invention can be used for the diagnosis, prognosis and treatment of e.g. cancers, inflammation, or demyelinating disease such as multiple sclerosis.
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detection; multiple sclerosis; demyelinating disease; myelin; ds.
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AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                          AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                            GAGAACCTGCGTGCAATCCATCTTGTTCAATGCGAAACGATCCTCATCCTGTCTTT
                                                                                            GAGAACCTGCGTGCAATCCATCTTCAATCATGCGAAACGATCCTCATCCTGTCTTT
                CGGTCTTGACAAAAAGAACCGGGGGCGCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
                                                                                                                                                                                                                                Breast cancer specific gene 1; BCGS1; human; metastasis; diagnosis;
therapy; genetic marker; vector; pHB3-4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of vector pHE4-5 that includes a neomycin phosphotransferase gene as selectable marker, an E. coli origin of replication from pUC19, a T5 phage promoter sequence, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human breast cancer specific gene - used to develop products for the diagnosis, clinical management and treatment of breast cancer and metastases
                                                                                                                    GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC
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Escherichia coli.
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lac operators, a Shine-Dalgarno sequence, and the lactose operon repressor gene (lacig). The newly isolated human breast cancer specific gene 1 (BCSP1, see AAV42669) can be operatively linked to the promoter and operator by insertion between the NdeI and Asp718 sites of the vector, allowing recombinant production of BCSP1 polypeptide (see AAW63123) in host cells. BCSP1 is useful as a breast cancer progressive marker. BCSP1 polymucleotides, polypeptides and antibodies can be used to develop products for the diagnosis, clinical management and treatment of breast cancer and metastasis.
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Sequence 1, Application US/08664224

Fatent No. 5851808

GENERAL INFORMATION:
APPLICANT: Elledge, Srephen J.
APPLICANT: Liu, Qinghua
TITLE OF INVENTION: Recombination
NUMBER OF SEQUENCES: 18
CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Median & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: United States of America
STATE: LBM FCO COMPATIBLE FCAM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSSIFICATION NUMBER: US/08/864,224
FILING DATE:
REGISTRATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: BCM-02681
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 397-8338
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US-09-620-647-4

US-09-620-925-3

US-09-920-925-3

US-09-30-190A-30

US-09-30-190A-30

US-09-30-190A-10

US-09-30-190A-10

US-09-380-190A-11

US-09-380-190A-11

US-09-380-190A-11

US-09-380-190A-11

US-09-380-190A-11

US-09-380-190A-11

US-09-380-190A-11

US-09-380-190A-17

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100.0%; Pred. No. 0;
tive 0; Mismatches
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2220 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Sequence 7, Appli
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Patent No. 5212080
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Sequence 16, Appl
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1: /cgni2_6/ptodate/2/ina/5A_COMB.seq:*

2: /cgni2_6/ptodate/2/ina/5B_COMB.seq:*

3: /cgni2_6/ptodate/2/ina/6A_COMB.seq:*

4: /cgni2_6/ptodate/2/ina/6B_COMB.seq:*

5: /cgni2_6/ptodate/2/ina/FUGC_COMB.seq:*

6: /cgni2_6/ptodate/2/ina/packfiles1.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                            569978 seqs, 220691566 residues
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/508,379
FILING DATE: 12-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 105,422
FILING DATE: 05-OCT-1987
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Best Local Similarity 100.0%;
Matches 1001; Conservative 0
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GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
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US-09-042-105-16

Sequence 16, Application US/09042105

Sequence 16, Application US/09042105

Patent No. 6040157

GENERAL INFORMATION:

APPLICANT: HU, JING-SHAN

APPLICANT: CAO, LIANG

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROW

MUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 NEW YORK AVENUE

CITY: WASHINGTON

STATE: DC

COUNTRY: USA
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                                440 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTTT
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                                                                                                                                                            RESULT 3
US-09-026-343-33
i Sequence 3) Application US/09026343
i Sequence 3) Application US/09026343
i Patent No. 600801B
i GENERAL INFORMATION:
i GENERAL INFORMATION:
i APPLICANT: CONAMAY, DAN W.
i APPLICANT: CONAMAY, TOAN W.
i TILE OF INVENTION: ELL2, A New Member of an ELL Family of TITLE OF INVENTION: RNA POlymerase II Blongation Factors CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
i ADDRESSEE: STERNEY KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
        GAGAACCIGCGIGCAAICCAICTIGIICAAICAIGGGAAACGAICCICAICCIGI
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                                                                                 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                       380 GAICAGAICTIGAICCCCTGCGCCAICAGAICCTIGGCGGC 340
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CITY: WASHINGTON
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/026,343
FILING DATE: Herewith
CLASSIFICATION ON THE SEB-1997
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: 29,021
REPERBNEY/AGENT INFORMATION:
APPLICATION NUMBER: 29,021
REPERBNES/COCKET NUMBER: 29,021
REPERBNES/COCKET NUMBER: 29,021
REPERBNES/COCKET NUMBER: 29,021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2560
TELEFRAX: (202) 372-2540
INFORMATION FOR SEQ ID NO: 33:
FENUTH: A974 base pairs
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
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STRANDEDNESS: both
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MOLECULE TYPE: CDNA
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US-09-026-343-33
        901
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3059 GACCGGCTTCCATCCGAGTACGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATG 3118
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                      481 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCTTTCGCTTGGTGGTCGAATG 540
                                                                                                                                                                                               3119 GGCAGGTAGCCCGATCAAGCGTATGCAGCCGCGCATTGCATCAGCCATGATGGATACTT
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                                                                                                                                           541 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT
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Patent No. 6075124
GENERAL INFORMATION:
APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN
INVMER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,856A
FLING DATE: HEREWITH
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/726,830
FILING DATE: 08-07-1996
FILING DATE: 07-07N-1995
FILING DATE: 21-APR-1995
FILING DATE: 21-APR-1995
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STATE: DC
COUNTRY: USA
ZIP: 20005-3934
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: PSTSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED
FILING DATE: 24-DEC-1997
CLASSIFICATION:
ATTORNEY-AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1000003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMA
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
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MOLECULE TYPE:
US-09-042-105-16
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3479 GAGAACCIGCGIGCAAICCAICIIGIICAAICAIGCGAAACGAICCICAICCIGICICII 3538
                                                                                                        CGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGGGGGTTCAG 3418
                                     3419 AGCAGCCGATTGTTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                           841 AGCAGCCGATTGTCTGTTGTCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                                                                                                            GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTTT
                                                                            781 CGGTCTTGACAAAAAAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                          961 GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
FILING DATE: 14-FEB-1995
FILING DATE: 14-FEB-1995
FILING APPLICATION NUMBER: US 08/461,195
FILING DATE: 03-JUN-1995
FILING DATE: 03-JUN-1995
FILING DATE: 03-JUN-1995
FILING DATE: 03-JUN-1995
FILING DATE: 33-ANG-1996
FILING APPLICATION NUMBER: US 60/023,852
FILING DATE: 33-ANG-1996
FILING APPLICATION NUMBER: US 60/039,045
FILING DATE: 23-FEB-1997
FILING DATE: 23-MAY-1997
FILING DATE: 23-MAY-1997
FILING DATE: 33-ANG-1997
FILING DATE: 13-ANG-1997
FILING DATE: 13-ANG-1997
FILING DATE: 13-ANG-1997
FILING DATE: 13-ANG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TINENE, STEVEN M.
APPLICANT: JINENEZ, PABLO
APPLICANT: JINENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RANDRICK, DONNA
APPLICANT: ARNORICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: COLEMAN, TINOTHY A.
APPLICANT: COLEMAN, TINOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: GRUBER, STENER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS: 148
CORRESPONDENCE ADDRESS: 148
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & POX. P.L.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 147, Application US/09023082A Patent No. 6077692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NEW
CITY: WASHINGTON
STATE: DC
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.034000
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-2600
FILEFRAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TWITH: 3974 base pairs
                                                                                                                                                      1488.0340006
                                                                                                                                                                                                                                                                                            TYPE: mucleic acid

// STRANDEDNESS: both

TOPOLOGY: both

// MOLECULE TYPE: CDNA

US-09-044-856A-7
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3359 CGGTCTTGACAAAAAGAACCGGGGGCCCCTGCGCTGACAGCCGGAACACGGCGCATCAG 3418
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                                                                                                                                                                                                                                                                  3419 ACCAGCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                                                                                                                                                                                              901 GAGAACCIGCGAGCGATCCAICTIGITCAATGAAAAAAAGGATCCICATCCIGICICII
                                                                                                                  781 CGGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGGCATCAG
                                                                                                                                                                                                                       841 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LI, HAODONG
APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: RUBEN, STEVEN M
APPLICANT: RUBEN, STEVEN M
APPLICANT: STORY MANAGER G III
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3539 GAICAGAICTIGAICCCCTGCGCCAICAGAICCTIGGCGGC 3579
                                                                                                                                                                                                                                                                                                                                                                                                                                        961 GATCAGAICTIGAICCCCIGCGCCAICAGAICCTIGGCGGC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem FC compatible
COMPUTER: Elem FC compatible
COMPUTER: Elem FC compatible
COMPUTER: Elem FC compatible
COMPUTER: Elem FC compatible
COMPUTER: Elem FC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,855A
FILING DATE: HEREWITH
CLASSIFICATION NUMBER: US 08/479,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTOMERY AGENT INFORMATION:
NAME: COMPATER FULLY
NAME: TEMPETER FOLICY
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: STEPFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERNCA/POCKET NUMBER: 1488.0340005
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09044855A Patent No. 6100389
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: both
TOPOLOGY: both
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US-09-044-855A-7
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US-09-044-855A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAACAGTTCGGCTGGCGCGCGCGCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA 480
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100.0%; Pred. No. 0;
ative 0; Mismatches
APPLICATION NUMBER: US 60/055,561
FILLING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEEFEF, ERIC K.
REGISTRATION NUMBER: 36,668
REFERENCE/DOCKET NUMBER: 1488.0360'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
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Best Local Similarity 100.
Matches 1001; Conservative
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MOLECULE TYPE: cDNA
US-09-023-082A-147
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON STATE: DC COUNTRY: USA
                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/078,670
FILING DATE: Herewith
CLASS/FICATION:
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/046,415
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REPERENCE/DOKKET NUMBER: 1488.093001
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-261
TELEPHONE: (202) 371-261
SEQUENCE CHARACTERISTICS:
LENGTH: 3374 base pairs
Patent No. 6143498
GENERAL INFORMATION:
APPLICANT: OLSEN, HENRIK S.
APLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0
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Best Local Similarity 100.
Matches 1001; Conservative
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STRANDEDNESS: both
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                                                                 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
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RESULT 8 US-09-078-670-4 ; Sequence 4, Application US/09078670

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NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REPERENCE POCKET NUMBER: 1488.0300002
TELEPRONE: 202-371-2600
TELEPRONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1001; 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-026-408-14
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Best Local Similarity
Matches 1001; Conserv
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CGAACAGTTCGGCTGGCGCGCGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA
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APPLICANT: Ni et al.

TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flippy disk
COMPUTER: Dippy disk
COMPUTER: DEADER FORM:
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRITARION NUMBER: US/09/026,408
FLING DATE: Herewith
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APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
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Patent No. 6303338
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Patent No. 6420116
GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
TITLE OF INVENTION: Antimicrobial Peptide
FILE REFERENCE: 1488.0930002
CURRENT APPLICATION NUMBER: US/09/627,154
CURRENT FILING DATE: 2000-07-27
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3359 CGGTCTTGACAAAAAAAACGGGGGGCCCCTGCGCTGACAGCCGGAACACGGGGGCATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DUAN, D. ROXANNE
APPLICANT: SHILATIFARD, ALI
APPLICANT: CONAMAY, JOAN G.
APPLICANT: CONAMAY, SONALD C.
TITLE OF INVENTION: ELL2, A New Member of an ELL Family o
TITLE OF INVENTION: RNA POlymerase II Blongation Factors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIF: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Blopy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/362,871
FILING DATE:
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Pred. No. 0;
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CCLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,343
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRANTON NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.08
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 371-2600
TELEFONE: (202) 372-2540
TELEFONE: (202) 372-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/09362871
Patent No. 6379923
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Best Local Similarity
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3479 GAGAACCTGCGTGCAATCCATCTTGTTCAATGCGAAAGGATCCTCATCCTGTCTCTT 3538
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Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1001; Conservative 0; Mismatches 0; Indels 0;
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OTHER INFORMATION: Description of Artificial Sequence: vector US-09-027-287-50
                                                                                                                               GAICAGAICTIGAICCCCIGCGCCAICAGAICCIIGGCGGC 1001
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APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: W. Guo-Liang
APPLICANT: W. Guo-Liang
APPLICANT: W. Guo-Liang
TITLE OF INVENTION: Apoptosis Inducing Molecule II
FILE REFRENCE: 1488, 0556004
CURRENT PELING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: US 09/027,287A
CURRENT PILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 08/822,953
EARLIER PELING DATE: 1996-01-07
EARLIER PELING DATE: 1996-01-07
EARLIER PILING DATE: 1996-01-31
EARLIER PELING DATE: 1996-11-31
EARLIER PILING DATE: 1996-11-31
EARLIER PILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PARCENTIN ONS: 55
                                                                                                                                                                                                                                                   Sequence 50, Application US/09027287A Patent No. 6479254
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ORGANISM: Artificial Sequence
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US-09-027-287-50
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100.0%; Score 1001,
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 09/078,670
PRIOR FILING DATE: 1998-05-14
PRIOR PILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 4
LENGTH: 3974
TYPE: DNA
CREANIN: SYNTHETIC CONSTRUCT
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2939 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG 2998
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                                  CGAACAGTICGGCTGGCGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA 480
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                                                               2999 CGAACAGTTCGGCTGGCGCGCGTGATGCTCTTCGTCCAGATCATCCTGATCGACAA
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APPLICANT: Nibbs, Robert J.B.
APPLICANT: CRAAM, Gerand J.
TITLE OF INVENTION: CHEMOKINE BETA-7
FILE REFERENCE: 1488.033000F
CURRENT APPLICATION NUMBER: US/09/437,602
CURRENT FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/107,801
PRIOR FILING DATE: 1999-11-10
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Patent No. 6495128
GENERAL INFORMATION:
APPLICANT: Salcedo, Theodora W.
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Matches 1001; Conservative
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APPLICANT: Gentz, Reiner L.

APPLICANT: Goldan, Timothy A.

TITLE OF INVENTION: Expression Control Sequences

FILE REFRENCE: PV447

CURRENT FAPLICATION NUMBER: US/09/044,796A

CURRENT FILING DATE: 1998-03-20

PRIOR PRILNG DATE: 1997-09-30

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR FILING DATE: 1998-03-20

PRIOR PLING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 09/044,796

PRIOR PLING DATE: 1998-03-20

PRIOR PRIOR DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 09/044,796

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; Patent No. 6194168
; GENERAL INFORMATION:
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APPLICANT: Ruben, Steven M.
APPLICANT: Zhang, Jun
APPLICANT: Zhang, Jun
APPLICANT: Lang, Jun
APPLICANT: Ulrich, Stephen
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REPERENCE: 1488.0663006
CURRENT APPLICATION NUMBER: US 60/075,409
FILO APPLICANTION NUMBER: US 60/075,409
FRIOR APPLICATION NUMBER: US 60/075,409
FRIOR APPLICATION NUMBER: US 09/027,287
FRIOR PLING DATE: 1998-02-20
FRIOR PLING DATE: 1998-02-20
FRIOR PLING DATE: 1998-01-07
FRIOR PLING DATE: 1998-01-07
FRIOR APPLICATION NUMBER: US 60/013,923
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FRIOR FILING DATE: 1996-10-31
FRIOR SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 1001, Conservative
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GREAKAL INFORMATION:
APPLICANT: Fompejus, Markus
APPLICANT: Frompejus, Markus
APPLICANT: Schroeder, Hartwig
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APPLICANT: Schroeder, Gregor
APPLICANT: Hacher, Schroeder, Gregor
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CURRENT PRILING DATE: 2002-11-29
CURRENT FILING DATE: 2002-11-29
FRICR APPLICATION NUMBER: 60/422618
FRICR APPLICATION NUMBER: 60/14269
FRICR APPLICATION NUMBER: 60/14269
FRICR FILING DATE: 1999-06-25
FRICR FILING DATE: 1999-06-25
FRICR FILING DATE: 1999-07-01
FRICR APPLICATION NUMBER: 60/14269
FRICR APPLICATION NUMBER: 60/14269
FRICR APPLICATION NUMBER: DE 1993-07-01
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FRICR APPLICATION NUMBER: DE 1993-07-08
FRICR APPLICATION NUMBER: DE 1993-07-08
FRICR APPLICATION NUMBER: DE 1993-07-08
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FRICR APPLICATION NUMBER: DE 1993-122.
FRICR PILING DATE: 1999-07-09
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FRICR FILING DATE: 1999-07-09
US-10-120-398-16
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US-10-090-983-1
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US-10-059-066-35
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Publication No. US20030162267A1
GENERAL INFORMATION:
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Sequence 14, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-973-726-16

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US-09-918-681-20

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seq length: 200000000
                                                                                                         February 15,
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Result No.

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APPLICANT: Klopprogge, Corinna
TITLE OF INVENTION: CORNVEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY
TITLE OF INVENTION: CORNVEBACTERIUM GLUTAMICUM GENES ENCODING REGULATORY
TITLE OF INVENTION: PROTEINS INVOLVED IN THE PRODUCTION OF METHIONINE
FILE REPERENCE: 807-11-29
CURRENT APPLICATION NUMBER: 09/602874
PRIOR APPLICATION NUMBER: 00/422618
PRIOR PILING DATE: 2000-06-23
PRIOR PELING DATE: 2000-10-30
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-01
PRIOR PLING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                  GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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LOCCATION: (457)..(1248)
OCCATION: kanamcyin resistance gene form In5
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/10307138 Publication No. US20030162267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kroger, Burkhard
Schroeder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
Haefner, Stefan
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ORGANISM: Artificial Sequence
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SEQ ID NO 15
LENGTH: 2772
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                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: vector
OTHER INFORMATION: pINTEGRATIV
                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc feature

LOCATION: (1515)...(2375)

OTHER INFORMATION: Ori from pMB for replication in E.coli
US-10-307-138-14
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                                                                                                                                                                                          FEATURE:
NAME/KRY: misc feature
NAME/KRY: misc feature
(1248)
OTHER INFORMATION: kanamycin resistance gene from ThS
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                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 100.0%; Score 1001; score 1001; Conservative 0; Mismatches
                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 1001; Conserva
                                         O ID NO 14
LENGTH: 2406
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610 CGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAG
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                                                                      GAGAACCIGCGIGCAATCCATCTIGTTCAATCATGCGAAACGATCCTCATCCTGTCTTT
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                                                                                                                                                                              GATCAGATCTTGATCCCTGCGCCATCAGATCCTTGGCGGC 1001
                                                                                                                                                                                                            GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 390
                                                                                                                                                                                                                                                                                       Sequence 50, Application US/09027287A
Sequence 50, Application US/09027287A
GENERAL INFORMATION:
APPLICANT: Enhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Rulen, Stewn M.
APPLICANT: Rulen, Stewn M.
APPLICANT: Rulen, Stewn M.
APPLICANT: TILICANT: 1488.0655004
CURRENT APPLICATION NUMBER: US/09/027,287A
CURRENT FILING DATE: 1998-02-0
GURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 09/033,886
EARLIER PILING DATE: 1999-03-21
EARLIER PILING DATE: 1999-03-21
EARLIER FILING DATE: 1997-03-21
EARLIER FILING DATE: 1997-03-31
EARLIER PILING DATE: 1996-10-31
EARLIER PILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATCHIN VET: 2.0
SEQ ID NOS: 55
LENGTHER PATCHIN VET: 2.0
SEQ ID NOS: 55
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(61)
OTHER INFORMATION: fragment of rxa02910 (cont. from bp 2772 in
OTHER INFORMATION: circular plasmid)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2407)...(2772)
OTHER INFORMATION: fragment of rxa02910 (1st part to be con. from bp
OTHER INFORMATION: 1 to 61 in circular plasmid)
                                                                                                                                                                                                                                                         DB 13; Length 2772;
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                                      for replication in
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NAME/KEY: misc_feature
LOCATION: (1515)..(2375)
OTHER_INFORMATION: Ori from pMB
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US-10-307-138-15
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100.0%; Score 1001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
                                                                                                       ; OTHER INFORMATION: PHE4-5 expression vector US-09-252-656B-50
                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                   PatentIn version 3.1
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 50
LENGTH: 3974
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APPLICANT: EDNEY, Reinhard
APPLICANT: EDNEY, Steven M.
APPLICANT: Yu, Guo-Liang
APPLICANT: Chang, Steven M.
APPLICANT: Chang, Jun
APPLICANT: Chang, Jun
APPLICANT: Chang, Jun
APPLICANT: Ulrich, Stephen
APPLICANT: APPLICANT: APOPLOSIS
ITLE OF INVENTION: 1880.055006
CURRENT APPLICATION NUMBER: US/09/252,656B
FILE REFERENCE: 1999-02-19
PRIOR APPLICATION NUMBER: US 60/075,409
PRIOR APPLICATION NUMBER: US 60/075,409
PRIOR APPLICATION NUMBER: US 09/027,287
PRIOR APPLICATION NUMBER: US 09/027,287
PRIOR PILING DATE: 1998-02-20
PRIOR FILING DATE: 1998-01-07
PRIOR PILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 08/023,953
PRIOR FILING DATE: 1998-03-21
PRIOR APPLICATION NUMBER: US 60/013,923
PRIOR FILING DATE: 1996-03-22
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Patent No. US20020127640A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09972912

Patent No. US20020110867A1
GENERAL INPORMATION:
APPLICANT: SOPET, DANIEL R.
TILLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 3974;
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COUNTRY: UC
COUNTRY: UC
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,912
FILING DATE: 10-Oct-2001
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: 09/049,022
FILING DATE: 4URHOWN>
APPLICATION NUMBER: 36/049,022
FILING DATE: 4URHOWN>
ATORNEY/AGENT INFORMATION:
NAME: SPEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,0001
TELECONTUNICATION INFORMATION:
MEDIATORIE PROPRATION: APPLICATION INFORMATION:
METERENCE/DOCKET NUMBER: 36,688
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-972-912-8
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
Matches 1001; Conserv
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US-09-972-912-8
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Publication.No. US20030008357A1
GENERAL INFORMATION:
APPLICANT: Hu, Jin.Shan
APPLICANT: Cao, Liang
APPLICANT: Cao, Liang
TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REFERENCE: PF112P3D1C1
CURRENT APPLICATION NUMBER: US/09/935,726
CURRENT PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/438,538
PRIOR PILING DATE: 1999-11-12
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                  601 TCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCC
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iive 0; Mismatches
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SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 3974
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US-09-935-726-16
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Best Local Similarity 100.
Matches 1001; Conservative
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US-09-935-726-16
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COURTRARE: DatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION BATA:
APPLICATION NUMBER: US/09/902,684
FILING DATE: 12-Jul-2001
CLASSIFICATION: CURROWN>
PILING DATE: 12-Jul-2001
FILING DATE: -CURROWN>
PILING DATE: -CURROWN>
APPLICATION NUMBER: US/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, BRIC K.
REGISTRATION NUMBER: 36,688
REFERENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-902-684-14
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pair
TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
Matches 1001; Conserv
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
                                                                                                                                                                                                    1488.0790001
       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,470
                                                                          PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 60/051,
FILING DATE: 27-UUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: STERFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 3974 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                             APPLICATION NUMBER: US
FILING DATE: Herewith
CLASSIFICATION:
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; MOLECULE TYPE:
US-09-105-470-25
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                                         GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC
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US-09-105-470-25
Sequence 25, Application US/09105470
Publication No. US20030022275A1
Publication No. US20030022275A1
APPLICANT: Carter, Kenneth C.
APPLICANT: He, Wei-Wu
TITLE OF INVENTION: Human NK-3 Related Prostate Specific TITLE OF INVENTION: Gene-1
NUMBER OF SEQUENCES: 30
CRESSPONDENCE ADDRESS:
ADDRESSEE: STERNE; KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCAGATCTTGATCCCCTGCGCCATCAGATCCTTGGCGGC 1001
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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100.0%; Score 1001; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGBNT INFORMATION:
REGISTATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.036000
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-371-260
TELEFAN: 202-371-260
TELEFAN: 202-371-260
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US-09-345-373-147
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                                                  1299 TGGCCAGCCACGATAGCCGCGCTGCCTCCTGCAGTCATTCAGGGCACCGGACAGGT
                                                                                                                                                781 CGGTCTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGCGGCATCAG
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-UN-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 61/039,045
FILING DATE: 23-MAY-1997
FILING DATE: 23-MAY-1997
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Publication No. US20030077695A1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
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DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , STEVEN M.
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MOORE, PAUL A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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APPLICANT:
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2939 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGG 2998
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                                                                                                                                                                                                                                                                                                                                          3119 GGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTT 3178
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                                                                                                                                                                                            481 GACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCTGTTTCGCTTGGTGGTCGAATG 540
     361 AGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCTTTGAGCCTGG 420
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                                                                                                 421 CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAA
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Publication No. US20040002449A1
GENERAL INFORMATION:
APPLICANT: Hastings, Gregg A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Meth1 and Meth2 Polymucleotides and Polypeptides
FILE REPRENCE: 1488.1070000
CURRENT APPLICATION NAMER: US/09/989,687
CURRENT PILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 126
SEQ ID NO 12
IENGTH: 3974
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US-09-989-687-12
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APPLICANT: Intela-Arispe, Luisa
APPLICANT: Astings, Greeg A.
APPLICANT: Ruben, Steven M.
APPLICANT: Trull, Stephen M.
APPLICANT: Trull, Stephen H.
APPLICANT: Trull, Stephen H.
APPLICANT: Fromwald, Jamen A.
APPLICANT: Terrett, Jonathan A.
TITLE OF INVENTION: Methl and Meth2 Polymucleotides and Polypeptides
CURRENT APPLICATION NUMBER: US/09/373,658
CURRENT APPLICATION NUMBER: US/09/373,658
SUTHENT APPLICATION NOS: 125
SOFTWARE: Patentin Ver. 2.0
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Delt, DB 11, Length 3974,
Best Local Similarity 100.0%; Pred. No. 0,
Matches 1001; Conservative 0; Mismatches 0, Indels 0)
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ORGANISM: Homo sapiens
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TYPE: DNA ORGANISM: Artificial Sequence
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Matches 1001; Conservative
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Sequence 50, Application US/10375680 Publication No. US20040009147A1 GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard APPLICANT: Yu, Guo-Liang APPLICANT: Ruben, Steven M

US-10-375-680-50

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APPLICANT: Ultrich, Stephen

PEPLICANT: Zhai, Yifan

TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of
FILE REFERENCE: 1488.065000B

FILE OF PREFERENCE: 1488.065000B

CURRENT PEPLICATION NUMBER: US/10/375,680

CURRENT FILING DATE: 2003-02-8

PRIOR APPLICATION NUMBER: US 60/360,234

PRIOR PLING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-260-270-4
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                                 CGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCGAACACGCGGGGGGGCATCAG 3418
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                                                                                            AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG 900
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CGGTCTTGACAAAAAAAACGGGGGGGCGCCTGCGTGACAGCCGGAACACGGCGGCATCAG 840
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/614,275
FILING DATE: 08-Jul-2003
CLASSIFICATION: <UNKNOWN>
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FC
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/105,470B
FILING DATE: 26-Jun-1998
APPLICATION NUMBER: US 60/051,080
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/POCKET NUMBER: 1488.0790001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-614-275-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/10614275; Publication No. US20040014668A1; GENERAL INFORMATION:
APPLICANT: Carter, Kenneth C.
He, Wei.Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 30
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                                                                                                                 AGCAGCCGATTGTTGTTGTGCCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                       3359 CGGTCTTGACAAAAAAAACCGGGCGCCCTGCGCTGACAGGCGGAACACGGCGGCATCAG
                                                                                                                                                             GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTTT
                                                                                                                                                                                           3479 GAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCATCCTGTCTCTT
                                                                                          841 AGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IITLE OF INVENTION: MYELIN OLIGODENDROCYTE GLYCOPROTEIN-LIKE PROTEIN (MOGP) AND METHODS OF USE
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0520001/EKS/RCM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFACK: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 NEW YORK AVENUE, NW, SUITE OCITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve:
CURRENT APPLICATION NAMBER: US/10/197,844
FILING DATE: 19-Jul-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,963
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/035,445
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
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100.0%; Pred. No. 0;
ive 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-197-844-9
                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10197844
) Publication No. US200310669981
GENERAL INFORMATION:

APPLICANT: CHOPRA, ARVIND
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ADDRESSEE: STERNE,
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Best Local Similarity 100.0
Matches 1001; Conservative
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US-10-197-844-9
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
         APPLICANT: GTADAM, GGETATO J. S.
TITLE OF INVENTION: CHEMOKINE BETA-7
FILE REFERENCE: 1488.033000F
CURRENT APPLICATION NUMBER: US/10/260,270
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US/09/437,602
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
SEQ ID NO 4
Nibbs, Robert J.B.
                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-260-270-4
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Best Local Similarity
Matches 1001; Conserv
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Search completed: February 15, 2004, 22:26:53 Job time : 425.484 secs

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AQ876152 V133H12 m
AQ875052 V120F5 mT
AQ876139 V133G10 m
AQ447775 mgxb0011E
                                                                                    February 15, 2004, 21:50:21; Search time 2636.53 Seconds (without alignments) 9227.587 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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	ACCI	ESSION	AQ8	76152	,		1	1		
	VER	VERSION	A08	76152.1	GI: 63	8839	9			
-	KEYWO	WORDS	SSS	, vmorede	GSS. Sancharomynes nerevis	a i va	iae (haker,	a yeart)		
_	Ö	ORGANISM	1 0	haromy	100	Cerevisiae		,		
	5		Euke	ryota;	Fungi	ABC	omycota; Sa	accharomycotina;	Saccharomycet	ycetes;
			Saco	haromy	cetales	s; Sa	ccharomycet	; Saccharomycetaceae; Saccharomyces	myces.	
-	REF	REFERENCE	-	(bases	1 to 78	(4)				;
	A		A C S S	s-Macdo Stages.	nald, P	, Ro	Ross-Macdonald, P., Roemer, T., Congress S.A., Cheung, KH., S.	∵ .	R., Agarwal,S., Symoniatis.D	Kumar, A., Jansen, R.,
-			Umar	sky, L,	, Heidt	man,	M., Nelson,	्र त्त	Kanada	
			Hage	er, K.,	Miller,	٠	Roeder, G.S.	der, G.S. and Snyder, M.		
_	H	TITLE	Larg	ge-Scal	e Analy	Bis	of the Yeas	by Tr	nosodsu	Tagging and
_	5	JOURNAL	Can	e pisru blishe	d d					
	COM		Cont	Contact: K	Kumar A					
_			Mich	ael Sn		Dept.	of Mol. Ce	Cell. and Dev. Bi	Biology	
-			100		08103	307	Haven, CT (06520-8103. IISA		
			. d		203 432 9949	<u>:</u>	5	1010 010		
_			Fax		32 6167					
			1	-						

Email: anuj.kumar@yale.edu

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Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales;
Saccharomycetales;
Saccharomycetales;
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Saccharomycetales;
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/note="Vector: pHSS6-Sal, A yeast genomic DNA library
without 2 micron or mitchondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mIn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="12278 - 2288C background, cir(0) rho(0)"
/db_rafe="taxon:4932"
/lab_host="E.coli"
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Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
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Best Local Similarity 100.0%; Pred. No. 5.7e-287;
Matches 568; Conservative 0; Mismatches 0;
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te of mTh.3xEA/LacZ insertion.
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class: transposon.tagged.
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AQ875052. GI:6287296
                                                                                                                                                                                                                                              /clone lib="wIn-3xHA/lacz Insertion Library, strain Y2278" Ante="Vector: pHSS6-Sal, A yeast genemic DNA library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of coughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mIn-3xHA/lacz minitransposon containing lacz, URA3, and tet resistance.
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/strain="Y2278 - 2288C background, cir(0) rho(0)"
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/lab_host="E. coli"
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100.0%; Pred. No. 5.6e-287;
ive 0; Mismatches 0;
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te of mTn-3xHA/lacz insertion.
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Class: transposon-tagged.
Location/Qualifiers
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AQ447775
mgxb0011E13f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
Clone mgxb0011E13f, genomic survey sequence.
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/clone="mgxb0011E13f"
/tissue_type="Protoplasts"
/lab_host="E. col PH10B"
/clone lib="CGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
                                                                                                                                                                                                                                                                                                                                        GCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGC 360
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Magnaporthe grisea
Bukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertea sedis; Magnaporthaceae; Magnaporthe.
10, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
              TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                              114 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT
                                                                                                                       GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAA
                                                                                                                                                                     374 GCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGCTCAGCCCATTCGCCGCCAA
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 655 5737
Fax: 864 656 4293
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/mol_type="genomic DNA"
/strain="70-15"
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 342.
Location/Qualifiers
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Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Bukaryota; Pungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.

It (bases 1 to 798)
Stoss-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Gestlages, S.A., Chempon, K., Iwasaki, H., Kanada, D., Jugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

In published
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
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strain Y2278 Saccharomyces
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                                CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCGTCGACAA
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CGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCGTCGACAA
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798 bp DNA line V133G10 mTn-3xHA/lacZ Insertion Library, strain erevisiae genomic 5', genomic survey sequence AQ876139
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/organism="Saccharomyces cerevisiae"
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Pred. No. 9.3e-262;
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Le of mTh-3xHA/LazZ insertion.
Seq primer: GGCCTTCTTTTTTTTGGAAGTAC
Class: transposon-taged.
                                                                                                                                                                                                                       GGCAGGTAGCCGGATCAAGCGTATGCAG
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/clone_lib="min-3xHA/lacz Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="vector: pHSS6-Sal; Benomic DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mIn-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
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BAC Library Magnaporthe grisea genomic
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/strain="Y2278 - S288C background, cir(0) rho(0)"
/db xref="taxon:4932"
/lab_host="E. col!"
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                                   Dept. of Mol. Cell. and Dev. Biology
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cerr.
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 949
Fax: 203 432 6161
Email: anuj. kumars@vale.edu
te of mrn-3xHA/lacZ insertion.
Seq primer: GGCTTCTTTTTGGAAGTAC
Class: transposon-tagged.
Location/Qualifiers
Location/Qualifiers
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of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
Bukaryota; Rungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetas; Saccharomycetas; Saccharomycetas.

1 (bases 1 to 790)
Sascharomycetals; Saccharomycetas.

1 (bases 1 to 790)
GesEtages; S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.

Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Unpublished
                                                                                                                                                                                                                                                                                                                                              449
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strain Y2278 Saccharomyces
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Vl32H11 mTn-3xHA/lacZ Insertion Library, strain
cerevisiae genomic 5', genomic survey sequence.
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100.0%; Pred. No. 1.8e-255;
ive 0; Mismatches 0;
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mgxb00006P12f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0006F12f, genomic survey sequence.
AQ398880
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                                                                                                                                                                                                                                                                                                                                                                                                                     660 AGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAAGGAACGCCCGTC 719
480 AGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAAT 539
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Magnaporthe grisea
Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina, Sordariomycetes;
Sordariomycetes incertea sedis; Magnaporthacea; Magnaporthe.

(bases 1 to 499)
Yu, Y. Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGGCACAGCTGCGCAAGGAACGCCGGTC 60
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
TEL: 864 656 5737
Fax: 864 656 4293
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/mol_type="genomic DNA"
/strain="70-15"
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Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Location/Qualifiers
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//issue_type="Totoplasts"
//issue_type="Totoplasts"
//lab_host="E_coli DH10B"
//clon=lib="Cudi Rice Blast BAC Library"
//clon=lib="Cudi Rice Blast BAC Library"
//clon=lib="Cudi Rice Blast BAC Library"
//clon=lib="Cudi Rice Blast BAC Library
//clon=lib="Cudi Rice Blast Bac Back Back Blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction.
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
//kpp was constructed. This library represents greater
than 25% genome coverage. High density colony filters
are available upon request."
3 others
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                                                                                                                                                                                                                                                                          1 (bases 1 to 789)
Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                                                   Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contract: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tal: 864 655 5737
Fax: 864 656 4293
   clone mgxb0005K01f, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rdeam@ollemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 41
High quality sequence stop: 392.
Location/Qualifiers
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/clone="mgxb0005K01f"
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/strain="70-15"
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AQ361914.1 GI:4211753
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/db_xref="(axon:148305")
/db_xref="(axon:148305")
/clone="mgxb0021821f"
/tissue_type="Protoplasts"
/lab_host="E_collBridge"
/clone_lib="CuGI Rice Blast BAC Library"
/note="Vector: pBACWICH, Site_l: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Magnaporthe grisea
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mgxb0023E21f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0023E21f, genomic survey sequence.
                                                                                                                   440
                                                                               235
                                                                                                                                              GCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCAC 295
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                  GGGCTGCGAATCGGGAGCGCGATACCGTAAAGAACGAGGAAGCAGTCAGCCCATTCGCC
                                                                                                                                                                    ACCAGACACAGACATCGATGAATCCAGAAAAGCGGCCATTTTCCACATGATATTCGG
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                                                                       GCGCTGCGAATCGGGAGCGGGTACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCC
                                                                                                                                                                                                                      ACCCAGCCGGCCACAGTGAATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGG
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                                            Gaps
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
       Length 499;
                                      Indels
                         9.3e-251;
       Score 499; DB 28;
                                                                                                                                                                                                                                                                                                                                                                 CCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Magnaporthe grisea"
/mol_type="genomic DNA"
49.9%; Score 499; DB
llarity 100.0%; Pred. No. 9.3
Conservative 0; Mismatches
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 395.
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AQ875040 861 bp DNA linear GSS 08-NOV-1999 V120E4 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces Grervialae genomic 5', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Bukaryota; Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Bukaryota; Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
1 (bases 1 to 861)
Rosse Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S., and Snyder, M.
Gene Disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="min-3xHA/lacz Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
was prepared in
pHSS6-Sal; genomic DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a min-3xHA/lacz
minitransposon containing lacz, URA3, and tet resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TCGAACCCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCT 180
                                                                                  64 TCAGCCATGATAGTTTCTCGGCAGGAGGAAGGTGAGTGACAGGAGATCCTGCCC
                         124 Troccirgeregregregategecageragecegarcaagegrarecagecegecegearreca
                                                          582 TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCC
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       /mol_type="genomic DMA"
/strain="Y2278 - S288C background, cir(0) rho(0)"
db_xref="taxon:1932"
/lab_host="E. coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 1.4e-247;
ive 0; Mismatches 0;
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Le of mTh.3XHA/LacZ insertion.
Seq primer: GGCCTTCTTTTTGGAAGTAC
Class: transposon-tagged.
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               Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                         Contact: Dean RA
Clemson University Genomics Institute
Clemson University
Il00 Jozdan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
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Pred. No. 1.4e-247;
0; Mismatches 1; Indels
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mol_type="genomic DNA"
strain="70-15"
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Class: BAC ends
High quality sequence stop: 291
Location/Qualifiers
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clone="mgxb0006009f"
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llarity 99.8%;
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AQ875907 801 bp DNA linear GSS 08-NOV-1999 V130H3 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
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Michael Snyder, Dept. of Mol. Cell. and Dev
Yale University
P.O. Box 208103, New Haven, CT 06520-8103,
Tel: 203 432 9949
                                                                                                                  <u>D</u>B
                                                                                                  Query Match
48.9%; Score 489; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 489; Conservative 0; Mismatches
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/mol_type="genomic DNA"
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/db xref="taxon.4932"
/lab_host="E. coli"
/lab_host="mn-3xHA/lacz Insertion Library, strain Y2278"
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te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGAAGTAC
Class: transposon-tagged.
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desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Sheehan, A., Symoniatis, D., Jansen, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M., Kanada, D., Lugo, R., Larges Scale Analysis of the Yeast Genome by Transposon Tagging and Unpublished
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100.0%; Pred. No. 3.2e-240;
ive 0; Mismatches 0;
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                                                                                                                        Concact: Kumar A
Michael Snyder, Dept. of Mol. Cell. a
Yale University
P.O. Box 208103, New Haven, CT 06520-
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mIn.3xHA/lac2 insertion.
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                                                  /organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="N2278 - 8288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
/lab_host="E.col;"
/lab_host="E.col;"
/clone_lib="mtn-3xHA/lacZ Insertion Library, strain Y2278"
/note="Vector: pK856-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in pH856-Sal; agenomic DNA was stare-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mtn-3xHA/lacZ
minitransposon containing lacz, URA3, and tet resistance.
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Saccharomyces cerevisiae
Eukarychz; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Baccharomyces.
1 (bases 1 to 783)
                                                                                                                                                                                                                                                                                                                                                                CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAACGATTCCGAAGCCCAACCTTTCATAG
                                                                                                                                                                                                                                                                                                                                                                                              CGCTGGAGGATCATCCAGCCGGCTCCCGGAAACGATTCCGAAGCCCTAACTTCATAG
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                                                                                                                                                                                                                                                                                                           Length 801;
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Pred. No. 2.9e-241;
0; Mismatches 1;
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              transposon-tagged.
Location/Qualifiers
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llarity 99.8%;
Conservative
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/tissue_rypes_Throplasts"
/lissue_rypes="Protoplasts"
/lissue_rypes="Protoplasts"
/lissue_rypes="Protoplasts"
/cloc lib="CGI Kice Bite 1: HindIII; Site 2: HindIII;
/note="Vector: pBAGNICH; Site 1: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
                                                                                                                                                                                                                                                                                                                                                                                                                        620 bp DNA linear GSS 06-MAR-1999 mgxb0009005f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0009J05f, genomic survey sequence.
AQ398387
GSS-8387.1 GI:4369414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Bukaryothe; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incerea sedis; Magnaporthaceae; Magnaporthe.

(bases 1 to 620)
Yu, Y. Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Saainowski, M. Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
     261 GATACTITCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCC
                                                                                                                                                                                     654 AATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACACGTGCGCAAGGAACG
                                                                                                                                                                                                                                   201 ANTAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACACGTGCGCAAGGAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC
Tel: 864 656 573
Fax: 864 656 4293
Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
46.8%; Score 468; DB 28; I
Best Local Similarity 100.0%; Pred. No. 1.9e-234;
Matches 468; Conservative 0; Mismatches 0;
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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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/clone="mgxb0009J05f"
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Location/Qualifiers
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/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/clon=11b="CudI Rice Bate BAC Library"
/roce="Vector: pBAGNICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous assomycete with
a haploid genome (la-7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fingal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request." 2 others
                           AQ447874 551 bp DNA linear GSS 08-APR-1999 mgxb0012101f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0012101f, genomic survey sequence.
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                                                                                                                                                                    Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Bukaryota, Fungil, Ascomycota, Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthacea; Magnaporthe.

[ bases 1 to 561)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M, Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: reaan@clemson.edu
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100.0%; Pred. No. 1.8e-234;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 42
High quality sequence stop: 326.
Location/Qualifiers
1. .51
/organism="Magnaporthe grisea"
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strain="70-15"
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Query Match Length DB ID 1674 100.0 1674 6 BD270607 1674 100.0 1674 6 BD270607 1674 100.0 1674 6 BD270607 1664.6 99.4 100.0 1674 6 BD134149 1664.6 99.4 2031 6 AR231261 1664.6 99.4 2031 6 AR231261 1663 99.3 2031 6 AR231262 1663 99.3 2031 6 AR231262 1663 99.3 2031 6 AR231261 1651.8 98.7 1997 6 AR211280 1651.8 98.7 1997 6 AR211281 1862.9 1.2 1997 6 AR211281 1862.8 1997 6 AR211281	otion	BD270667 Vascular AR381510 Sequence BD001745 Human vas BD134149 Vascular BC035212 Homo sapi AR231261 Sequence AR341826 Sequence BC063685 Homo sapi	AR231262 Sequence AR342827 Sequence AR112510 Sequence AR157589 Sequence BD247178 USe of VE AR201986 Sequence AR212635 Sequence AR430033 Sequence AR430033 Sequence AR4300371 Sequence	6 Sequence 9 Vascular H.sapiens m Human vascular Human FLT4 8 Vascular 0 Vascular 5 Bos tauru 9 Sequence	USALLZ MUS MUSCULU U73620 Mus musculu AR112511 Sequence AR2012641 Sequence AR430039 Sequence AR430039 Sequence BD082160 Vascular AR157586 Sequence AF42867 Meriones Y15837 Coturnix co AR112512 Sequence AR201988 Sequence BD082161 Vascular AC03801 Homo sani	1 L N 00 E	Vertebrata, Euteleostomi; 1; Hominidae, Homo. chke, V. and Ruben, S.M.
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HUMAN GENOME SCIENCES INC
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PD 19-N0V9-2002
PF 07-FEB-2000 JP 2000596954
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Human vascular endothelial growth factor 2.

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Homo sapiens (human)

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CRAIGA ROSEN, LIANG KAO, JIN SHAN FU

PC CL2N1/21, A61K38/22, A61K48/00, A61P9/10, A61P9/12, A61P17/06, PC

A61P19/02,

PC CO7K14/50, CO7K16/22, C12N5/10, C12N15/09, C12Q1/68, C12Q1/70, PC

A61K37/24,

PC C12N5/00, C12N15/00

CC Strandedness: Double;

CC Topology: Linear;

CC Vascular endothelial growth factor 2

PH Rey

PT Sig_peptide 12.80

FT mat_peptide 12.80

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100.0%; Score 1674; DB 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1674; Conservative 0; Mismatches 0;
                                                                                                                                                                                                           unidentified
unclassified.
1 (bases to 1674)
Rosen,C.A., Kao,L. and Fu,J.S.
Rosen,C.A. 2002505873-A 1 26-FEB-2002;
HUMAN GENOME SCIENCES INC
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BD134149
Vascular endothelial growth factor
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unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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   LOCUS
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                                                                             /Olone="MGC:24887 IMAGE:4753457"
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                                                                                                                                                                                                                                                                                                                                                                                                            'codon_start=1
'product="vascular endothelial growth factor
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/note="PDGF; Region: Platelet-derived
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99.7%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)

Ebkaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryofa, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

Elkaryofa, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

Straubberg, R.D., Pelngold, B.A., Grouse, L.H., Derge, J.G.

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Parmer, S.I., Wangy J., Hsieh, F., Diatchenko, L., Marusina, K., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Bosak, S.B., McBwan, P.J., Abrange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Malek, J.A., Gundiano, N.A., Peters, G.J., Abramson, R.D., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Wilalon, D.K., Marzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madah, A., Ketteman, M., Madah, A., Koliguez, A.B., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schlutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                     BC035212 1948 bp mRNA linear PRI 07-CCT-2003 Homo sapiens vascular endothelial growth factor C, mRNA (cDNA clone MGC:24887 IMAGE:4753457), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 29 Row: k Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19924300. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ.
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Submitted (31-UUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                  1561 Africatifitrahaggaagagaatiggraaaactgagtgatgargartritatatgar
                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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TITLE JOURNAL

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FEATURES

AUTHORS

MEDLINE PUBMED REFERENCE

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Qy 1621 GCAAATTATTTAAAATGAAATTGAAATTGTATTATAAAAAAA		ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 2031) AUTHORS Lee,J. and Wood,W. TITLE VEGF-related protein JOURNAL Patent: US 6451764-A 1 17-SEP-2002; FEATURES SOURCE 12031 /organism="unknown" /mol_type="genomic DNA"	Query Match 99.4%; Score 1664.6; DB 6; Length 2031; Best Local Similarity 99.8%; Pred. No. 0; Matches 1667; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	OY 1 GICCITCCACCAIGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGCTCGCCGC	Qy 61 CGCTGCTCCCGGGTCCTCGCGAGGCCCCGCCGCCGCCGCCTTCGAGTCCGGACTCG 120 L	QY 121 ACCTCTCGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 181 AGGACAGTTACGGTCTGTGTCTCCAGTGTAGAACTCATGACTGTACTCTACCCAGAAT 240 Db 541 AGGACAGTTACGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT 600	QY 241 ATTGGAAAATGTACAAGCTAAGGAAAGGAAAGGTGGCAACATAACAGGAACAGG 300 DD 601 ATTGGAAAATGTACAAGTCTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAAACAGG 660	Oy 301 CCAACCTCAACTCAAGAACAGAAGACTATAAAATTTGCTGCAGCACATTATAATAAGA 360	Qy 361 AGATCTTGAAAAGTATTGATAATGAGGAGAAAAGACTCAATGCATGC	Qy 421 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG 480	QY 481 TGTCCGTCTACAGATGTGGGGGGTTGCTGCAATAGTGAGGGCTGCAGTGCATGCA	2y 541 GCACGAGCTACCTCAGCAACACGTTATTTGAAATTACAGTGCCTCTCTCT	Qy 601 AACCAGTAACAATCAGTTTTGCCAATCACATTCCTGCCGATGCATGTCTAAACTGGATG 660
735 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACC 794 541 GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCT	AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG	1 NGCARCGARCAAGACCTGCCCCACCTTACATGGAATAATCACATCTGCAGATGCC 780 975 AGGCAGCGAACCAGCCCCACCATTACATGGAATAATCACATCTGCAGATGCC 780 975 AGGCAGCGAACCAGACCTGCCCCACCATTACATGGAATAATCACATCTGCAGATGCC 1034 781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGCATTCC 840 1035 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGACGAGACTCCAACAGATGCATTCC 1094 841 ATGACATCTGTGGACCAAACAAGAGGAGCTGGATGACCTGTCAGTGTCTCGCAGAG 900 1095 ATGACATCTGTGGACCAAACAAGAGGACTGGATGAAGACCTGTCAGTGTCTGCAGAG 1154	55		1021 ACACATGCCAGTGTGTAAAAAAAACTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080 	1081 AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC 1140 	1141 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC 1200 	1201 CAGGATTITCATATAGIGAAGAAGIGIGICGITGIGCCCTICATAIIGGCAAAGACCAC 1260 	1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT 1320 	1321 TGCCACAGTAGAACTGTCTGTGAACAGAGACCCCTTGTGGGTCCATGCTAACAACAAAGACA 1380 	1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGGTCATCTG 1440 	1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAAAGAGCCAAGATTTTCCTC 1500 	1501 TIGIGATTICITTAAAAGAATGACIATATAATTITATTICCACIAAAAATATIGITTCIGC 1560 	1561 ATTCAITTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT 1620

DEFINITION Sequence 1 from patent US 6576608. ACCESSION AR342826.1 GI:33738052 KERYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (Dases 1 to 2031) AUTHORS Lee, J. and Wood W. TITLE Methods of using VEGF-related protein JOURNAL Patent: US 6576608-A 110-JUN-2003; FEATURES 1. 2031 SOURCE 1. 2031 ACCEPTABLE NOTE 1 LOCATION/QUALIFIERS 1. 2031 ACCEPTABLE NOTE 1 LOCATION/QUALIFIERS ACCEPTABLE NOTE 1 LOCATION/QUALIFIERS ACCEPTABLE NOTE 1 CONTROLLE NOTE 1	Query Match 99.4%; Score 1664.6; DB 6; Length 2031; Best Local Similarity 99.8%; Pred. No. 0; Matches 1667; Conservative 0; Mismatches 4; Indels 0; Gaps 1 GTCCTTCCACCATGCACTCGCTGGCTTTCTCTGTTCTCTGTCGCGCTGT	OY	OY 121 ACCTCTGGACGCGGAGCCCGACGGGCGCACGGCTTATGCAAGCAA	OY 181 AGGAGAGTTACGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT 240	Oy 241 ATTGGAAATGTACAAGTGTCAAGGAAAAGGAGGCTGGCAACATAACAGAAAGAGG 300	Oy 301 CCAACCTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG 360	OY 361 AGATCTTGAAAAGTATTGATAATGAGTAGAGAAAGACTCAATGCATGC	Qy 421 GTATAGAIGIGGGGAAGGAGTITIGGAGTCGCGACAACACCTTCTTTAAACCTCCATGTG 480	QY 481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGAACACCA 540	OY 541 GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCT	QY 601 AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG 660	Qy 661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACAACTACCACAGTGTC 720 1021 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 1080	OY 721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780
661 TITACAGACAAGITCATTCCATTATTAGACGTTCCCTGCCAGCAACTACCACCAGTGTC 720 1021 TITACAGACAAGITCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720 1021 TITACAGACAAGACCTGCCCCACTATTACATGTGGAATAATCACATTGCAGATGCC 780 721 AGGCAGCGAACAAAAAACTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780 1081 AGGCAGCGAACAAAAAATTTTCCTCGAATGCAATAAATCACATGAATGCATTCC 840 1141 TGGCTCAGGAAGATTTTATGTTTTCCTCGAATGCAATACAATGCAATTCC 1200 841 ATGACATCTGTGGAACAAAAAAGGAGCTGGATGAACACATGCAATGCAATCC 1200 841 ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAACACTCTCACAGATGCAATCC 7200 1201 ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAACACTCTCACAGATGCAATCC 7200 1201 ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAAGACCTGTCAGTGTGTCTGCAGAG 7260	901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTTAGACAGAAACTCATGCCAGT 960 1261 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAGAACTAGACAGAAACTCATGCCAGT 1320 961 GTGTCTGTAAAAACAACTCTTCCCCAGCCAATGTGGGGCCAACCGAAAAAAAA	ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCGAGAATTAAAATGAACCTGCCCAGAAATCAACCCCTAAAATCAACCAGAAATCAACCAGTGTGTAAAAAGAAACTGCCCCAGAAATCAACCAGTGTGTATGTA	1081 AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAA	1141 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACGGCCAGAAGGCTTGTGAGC 1200	1201 CAGGATTTTCATATAGTGAAGAGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC 1260 	1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATGATTTTCTATTATGGAAAACTGTGT 1320 	1321 TGCCACAGTAGAACTGTCTGTGAACAGACACACTTGTGGGTCCATGCTAACAAGACA 1380 	1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTTGAAGCTCATCTG 1440 	1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC 1500	1501 TIGIGATITCITIAAAAGAAIGACTAIAJAATITAITICCACTAAAATAITGITICUGC 1560 	1561 ATTCATTTTATAGCAACAATTGGTAAAACTCACTGTGATGAATATTTTATATGAT 1620 	1621 GCAAAATATGTITAAAATAAAATGAAAATTGTATTATAAAAAAAA	77 1926 1826 AR342826 2031 bp DNA linear PAT 17-AUG-2003
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Alaschar, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Saares, M.B., Bondldo, M.F., Casavant, T.L.,
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Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, B., Retteman, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Generation and initial analysis of more than 15,000 full-length
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Contact: MGC help desk
Email: cgapbs-ramaali.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I:M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Maryland;
Web sites http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: N. Boufsely.R., Bronky. Brooks, S.,
Blakesley,R.W. Bockstrom-Sternberg,S.M., Bronky.,
Blakesley,R.W. Bockstrom-Sternberg,S., Guan,X., Gupta,J., Hadpidhi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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TEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKBFGVATNTFFKPPCVSVY
RCGGCCNSEGLQCMYSTSYLSKTLFEITVPLSQGPKPVTISFANHTSCRCMSKLDVY
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19924300. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R. Direct Submission Submitted (08-DEC-2003) National Institutes of Health, Mammalian Submitted (08-DEC-2003) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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| Organism="Homo sapiens"

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| Mol_xref="teaxon:9606"

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| Clone="WGC:74703 IMAGE: transitional cell papilloma"

| Clone | Ibb="NIH MGC_93"

| Ab host="DH10B"

| Ind host="DH10B"
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AUTHORS
TITLE
JOURNAL
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PUBMED
          AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2076)
                                                        1141 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCCAACAGATGGATTCC
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       TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
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Query Match Best Local Similarity 99.7%; Pred. No. 0; Matches 1666; Conservative 0; Mismatches 5; Indels 0; Gaps 0; I GTCCTTCCACCATGCACTGGGGTTTCTTCTGTGGGGTGTTCTCTGGCGGGTG 60 1671 GTCTTCCACTGGAGTTCTTTTCTTTGTGGGGTGTTCTTCTGGCGGTGTTCTTC	ACCTCTCGGACGCGGAGGCGGGGGGGGGGCGGCGGGGGGGG	1491 AGGAGLAGITACGGIGICGGGGGGAAAGGAAAGCTCATGACTGTACTCTACCCAGAAT 1432 241 ATTGGAAAATGTACAAGTGTCACGTAAGGAAAGGAGGCTGGCAACATAACAGAAAAGGAGG 300 1431 ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAAAAAAGGAGG 1372 301 CCAACCTCAACTCAAGGACAGAAGAAGAACTATAAAAATTTGCTGCAGCACACATAAAAAAAA	AGAICTTGAAAAGTATTGATAATGAGTGGAGAAAAGACTCATGAGTGCCAGGGAGGTGT	1251 GTATAGATGGGGGAAGGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG 1192 481 TGTCCGTCTACAGATGTGGGGGTTTGCTGCAATAGTGAGGGGCTGCAGTGAACACCA 540 1191 TGTCCGTCTACAGATGTGGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGAATGACCA 1132 541 GCACGAGCTACCTCAACAAGATTTGAAATTACAGTGCTCTCTCT		721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATTAACATCTGCAGATGCC 780	901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATCCCAGT 960

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peripheral arterial disease; critical limb ischaemia; coronary disease;
angiogeneels; tumour; inflammation; diabetic retinopathy; psoriasis;
rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
infectious disease; neurodegeneration;
vascular endothelial growth factor-B; VEGF-B; ds.
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This sequence encodes vascular endothelial growth factor-B (VEGF-B),
which is an angiogenic protein of the invention. The angiogenic proteins
and the DNA sequences encoding them, are used to prevent, treat or
ameliotate disease and to detect diseases, or susceptibility, by
centecting mutations or the presence or amount of angiogenic protein
contecting mutations or the presence or amount of angiogenic protein
contecting mutations or the presence or amount of angiogenic protein
contecting material disease, critical limb ischaemia or coronary disease.
Contipheral arterial disease, critical limb ischaemia or coronary disease.
Contagonists of the sequences are used to inhibit angiogenesis in tumours
and to treat inflammation (where associated with increased vascular
contagonists are also useful for stimulating (lymph) angiogenesis. The
Agonists are also useful for stimulating (lymph) angiogenesis.
Conterapeutic agents) and to raise antibodies. The antibodies are useful as
therapeutic agents) and to raise antibodies. The artibodies are useful
conterpring of colls, for detection, purification and targeting of
therapeutic progenitor/stem cells. It is also contemplated that the
contemplates might be useful for treating a very wide range of other
contemplates might be useful for treating a very wide range of other
discorders, e.g. autoimmune diseases; allergy; cancer; infectious diseases
contemplated agents or for stimulating regeneration, also as
contemplated or parasitic); neurodegeneration, also as
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                                                                                               New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limbischemia or coronary disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; vascular endothelial growth factor 2; VEGF-2; gene; ss; pVGI.1; chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; allergic reaction; organ rejection; inflammatory condition; arrhythmia; hyperproliferation; orrhythmia; fungal infection; parasitic infection; cardiovascular disorder; embolism; heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid having expression vector construct with vascular endothelial growth factor-2 insert, useful for treating chronic limb ischemia or myocardial ischemia, autoimmune disorders and allergic conditions.
                                                                1561 ATTCATTTTTATAGCAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
                                                                                                                                BP; 501 A; 383 C; 376 G; 414 T; 0 U; 0 Other;
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P-PSDB; AAU76812.
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	SCAAGCAAAGATCTGG 18 STACTCTACCCAGAAT 24 		GGAGGTGT GGGAGGTGT	421 GTATAGAIGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTAAACCTCCATGTG 480	TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACAAAATTACAGTGCTGCAGTGCATGAACACCAAGGCCCCAACAGGGCTCTCTCT	601 AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTGTAAACTGGATG 660	661 TITACAGACAAGITCAITCCAITATAGACGITCCCIGCCAGCAACACIACCACAGGTC 720 	721 AGGCAGCGAACAAGACCTGCCCCCCCACCAATACATGTGGAATACATCTGCAGATGCC 780	rgactcaacagatggattcc 	841 ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGGACCTGTCAGTGTGTCTGCAGG 900 	901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGAAACTCATGCCAGT 960 	961 GTGTCTGTAAAAGAAACTCTTCCCAACCAATGTGGGGCCAACCGAGAATTTGATGAAA 1020 	1021 ACACATGCCAGTGTGTATATAAAGAACCTGCCCCAGAAATCAACCCTAAATCTGGAA 1080

(HUMA-) HUMAN GENOME SCI INC

Wager RE; Rosen CA, Albert VR, Ruben SM,

2003-092991/08

P-PSDB; ABJ19819

New isolated polynucleotide encoding an antibody which inhibits a VEGF-2 polypeptide, useful for diagnosing, treating or preventing diseases associated with aberrant VEGF-2 expression or function, e.g. cancer or inflammation.

Disclosure, Fig 1, 425pp, English.

The invention relates to an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody comprising an amino acid sequence selected from at least one, two or three CDR region(8) of a VH or VL domain where the first antibody or three CDR immunospecifically inhibits a VEGF-2 polypeptide. The isolated polynucleotide is useful in diagnosing, treating preventing, prognosing, aneliorating or monitoring diseases associated with aberrant VEGF-2 or VEGF-

Sequence 1674 BP; 501 A; 383 C; 376 G; 414 T; 0 U; 0 Other;

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1020 961 GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGGCCAACGGAATTTGATGAAA 1020 ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCAGAAATCAACCCCTAAATCCTGGAA 1080 1021 ACACATGCCAGTGTGTATGTAAAAAACTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080 1081 AATGTGCCTGTGAAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAAGAAGTTCC 1140 1081 AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC 1140 1200 1380 1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTTCTGCCAATGACCAAAACAGCCAAGATTTTCCTC 1500 1501 TTGTGATTTCTTTAAAGAATGACTATATAATTTTTTTCCACTAAAATATTTCTGC 1560 1561 ATTCATTTTTATAGCAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT 1620 1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTTCTATTATGGAAAACTGTGT 1320 1440 960 660 099 720 720 780 780 840 840 900 481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 540 481 TGTCCGTCTACAGATGTGGGGGTTGCTAATAGTGAGGGGCTGCAGTGCATGAACACCA 540 **AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG** 901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAAAAACTAGACAGAAACTCATGCCAGT 1201 CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC AACCAGTAACAATCAGTTTTGCCAATCACACTTCTGCCGATGCATGTCTAAACTGGATG TITACAGACAAGTICATICCATTATIAGACGTICCCIGCCAGCAACACTACCACAGIGIC 661 TTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACTAGTGTC AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 781 resercassasaririrarsiririceressarscressasarsacieaacasasarse <u>ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG</u> GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGGCCAACCGAGAATTTGATGAAA 1141 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGGCCAGAAGGCTTGTGAGC 1201 CAGGATTITICATATAGRAGAAGTGTGTGGTTGTGTCCTTCATATTGGCAAAGACCAC 1261 AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTG TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA 1321 reccacacrataga crerererea acacacacacerrerecerecare cranaca a de constante de c 1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG 1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGTCATCTG 1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC 1501 TIGTGATTTCTTTAAAAGAATGACTATATAATTTATTTTCCACTAAAAATATTGTTTCTGC TGGCTCAGGAAGATTTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTTCC 901 decedentececereceachergaaceceacaaagaachacaagaaanchenecac 1141 ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC 601 601 661 721 721 781 841 961 1021 d ò 셤 d g 셤 g g g g à à à ઠે g ò q à ò g à 유 ò 쉱 ð g δ g ò à à 8 ð ò ò

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This invention describes a novel isolated polymucleotide encoding a first antibody comprising an amino acid sequence selected from at least one, two or three complementarity determining (CDR) region(s) of a VH and/or U. Ondain of a second antibody that immunospecifically binds to a vascular endothelial growth factor (VBGF)-2 polypeptide. The products of the invention have cytostatic, cardiovascular, antirhemmatory, antiarhitic, antidabetic, ophthalmological, antimizammatory, antiarhitic, antidabetic, ophthalmological, antimizammatory, antiarhitic, antidabetic, ophthalmological, antiproviation actually. The polymucleotide is useful in diagnosing, cardiant, antialleragic, immunosuppressive, dermatological and antipsoriation actually. The polymucleotide is useful in diagnosing, treating, preventing, prognosing, ameliorating or monitoring diseases usociated with aberrant VBGF-2 or VBGF-2 receptor expression or lack of VBGF-2 or VBGF-2 receptor function, such as cancer and other profiterative disorders, cardiovascular disorders (arrhythmiss), offerious diseases, autoimmune diseases (e.g. rheumatoid arthritis, systemic Lupus Brythematosus, allergies), diabetic retinopathy or the invention may also be used to stimulate angiogenesis, wound healing, and promoting vascular tissue repair. The polymucleotide and polypeptide and promoting vascular tissue repair. The polymucleotide and polypeptide may also be used to stimulate angiogenesis, wound healing, and promoting vascular tissue repair. The polymucleotide and polypeptide of may also be used for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors and for the production of diagnostics and therapeutics e.g. gene therapy and in vaccines to treat
                              1561 ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTATATGTT 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; VH domain; VL domain, vascular endothelial growth factor; VBGF-2; cytostatic; cardiant; cardiovascular; antinflammatory; antinheumatic; antinfarthitic; antidiabetic; ophthalmological; antiallergic; vulnerary; immunosuppressive; daracological; antipsoriatic; proliferative disorder; cancer; cardiovascular disorder; arrhythmia; cerebrovascular disorder; cerebral anoxia; inflammatory disease; infectious disease; angiogenesis; autoimmune disease; Systemic Lupus Erythematosus; wound healing; vascular tissue repair; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide encoding an antibody which inhibits vascular endothelial growth factor (VEGF)-2 polypeptide, useful for diagnosing or treating diseases associated with aberrant VEGF-2 expression or function,
Rosen CA, Albert VR, Ruben SM, Wager RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1A-B; 344pp; English.
                                                                                                                                                                                                                                                          ABQ76966 standard; cDNA; 1674 BP.
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human diseases. This sequence encodes a polypeptide described in the disclosure of the invention
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                                                Seguence 1674 BP; 501 A; 383 C; 376 G; 414 T; 0 U; 0 Other;
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Matches 1674; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human vascular endothelial growth factor (VEGF-2) cDNA.
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The invention relates to vascular endothelial growth factor (VEGF)-2 antibodies are useful for treating, preventing or amalibodies. VEGF-2 antibodies are useful for treating, preventing or disorders, such as inflammatory diseases or disorders, proliferative disorders, tumours, tumour metastasis, breast cancer, brain cancer, prostate cancer, colon cancer. Implandation, an infectious disease, Kaposi's sarcoma, an autoimmune disease, rheumatoid arthritis, psoriasis, diabetic retinopathy, a disease or disorder associated with the lack of VEGF-2 (receptor) function. The disorder associated with the lack of VEGF-2 (receptor) function. The monitoring cancers and other hyperproliferative disorders. VEGF-2 is also used in gene therapy. The present sequence is human VEGF-2 cDNA
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                                                                                                                                                                                                                                                                                                                                                                        New vascular endothelial growth factor (VEGF)- 2 antibodies, for treating, preventing or ameliorating a disease or disorder, such as inflammatory diseases, proliferative disorders, autoimmune disorders or
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                                     /product= "Human mature VEGF-2 protein"
                                                                                                                                                                                                                                                                                 Wager RE;
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                                                                                                                                                                                                                                                                                 Albert VR, Ruben SM,
                                                                                                                                                12-APR-2002; 2002WO-US011404.
                                                                                                                                                                                    13-APR-2001; 2001US-0283391P.
07-SBP-2001; 2001US-0317600P.
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codes for human vascular endothelial growth 78), a protein structurally related to the capable of inducing angiogenesis in vivo. It was rary derived from early stage human embryo week may also be obtd. from adult heart or several . VEGF2 nucleic acids can be used in the prodn. probes to detect mutations in the VEGF2, and in
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gene therapy to treat patients in need of VEGF2. Antisense sequences be used as VEGF2 antagonists e.g. to inhibit growth of tumours
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                                     Seguence 1674 BP; 502 A; 384 C; 375 G; 413 T; 0 U; 0 Other;
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99.6%; Score 1667.6;
Best Local Similarity 99.8%; Pred, No. 0;
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                                                                                                                                                                                                                                                                                            protein similar to vascular endothelial growth factor - used to e.g. wounds, tumours, rheumatoid arthritis, Kaposi's sarcoma etc
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99.8%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA clone codes for human VEGF-C (AAW00932), a novel ligand that binds specifically to human Flt4 receptor tyrosine kinase (VEGFR-3), etimulating phosphorylation of the receptor, and which can be used to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases. The clone was isolated from a PC-3 prostatic adenocarcinoma cell (AYCC CRL 1435) CDNA library by PCR amplification and has been cloned into pcDNAI to form plasmid pFLT4-L (ATCC 97231). The human VEGF-C gene is located on chromosome 4q34 and contains 6 introns (see AAT84303-14). The insert from the human clone was used to isolate mouse (see AAT84277) and quail (see AAT84300) VEGF-C sequences. It can also be used to produce recombinant VEGF-C polypeptides in host cells and to provide probes for screening endothelial cell diseases. Antisense concluse that block the receptor can be used to control endothelial cell proliferation, e.g. lymphangioma or metastatic cancer. The promoter sequence (AAT84278) is also claimed
                                                                                                                                                                     VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; human; vascular endothelial growth factor receptor-3; ligand; angiogenesis; wound healing; lymph vessel; lymphangioma; cancer; metastasis; therapy; diagnosis; plasmid pFLT-4-L; ss.
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         Human Flt4 receptor tyrosine kinase ligand VEGF-C cDNA
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Pred. No. 0;
0; Mismatches
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ilarity 99.9%;
Conservative
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The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing yeacular permeability, and affecting myelopoiesis. The products can be used for stimulating angiogeneses, for inhibiting angiogenesis, for stimulating lymphangiogeneses, for inhibiting of inflammation, oedema, elephantiasis, or Milroy's disease. They can also be used for modulate myelopoiesis, e.g. treating granulocytopenia. They can also be used for modulating the growth of endothelial cells. They can also be used to stimulate lymphocyte production and maturation, and to promote or inhibit trafficking of leucocytes between tissues and lymphatic vessels or to affect migration in and out of the thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGCTCCCGGGTCCTCGCGAGGCGCCCGCCGCCGCCGCCGCCTTCGAGTCCGGACTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1997;
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99.9%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                          Example 10; Page 112-115; 177pp; English
                              LUDWIG INST CANCER RES.
UNIV HELSINKI LICENSING LTD.
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Matches 1653; Conservative
                                                                                      Alitalo K, Joukov V;
                                                                                                                           WPI; 1998-437470/37.
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ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCAGAAATCAACCCCTAAAATCTGGAA
                            AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
                                                                                                                                                                                                                               CAGGATTTTCATATAGTGAAGAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
                                                                                                                                                                                CAGGATTTTCATATAGAGGAGGGGTGTCGTTGTGCCTTCATATTGGAAAAAACACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
                                                                                                                                                      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
                                                                                                                                                                                                                                                                                                                                                   Flt4, vascular endothelial growth factor C; vascular endothelial cell; lymphatic endothelial cell; myelopoiesis; angiogeneses; inflammation; lymphangiogenesis; oedema; elephantiasis; Milroy's disease; ss.
                                                                            AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
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                                                                                                    Vascular endothelial growth factor-C, VBGF; human; re-endothelialisation; vascular endothelial growth factor receptor; VBGFR; vascular trauma; blood vessel; cardiovascular surgery; anti-restancsis agent; prevention; restencess; stencess; percutaneous transluminal coronary angioplasty; ss.
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/note= "Encodes carboxy terminal peptide, which on
cleavage results in partially-processed VEGF-C protein"
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                                                                                                                                            Screening a human subject for increased risk of developing a lymphatic disorder, comprises assaying a nucleic acid to determine a mutation altering the sequence of a vascular endothelial growth factor receptor-3.
                                                                                                                                                                                                                                                   The present sequence is the coding sequence for the human vascular endothelial growth factor ( (VGF-C). It was used to demonstrate the methods of the invention, which involve the screening of individuals to determine which vascular endothelial growth factor receptor 3 (VBGFR-3, also known as Flt4 or fms-like tyrosine kinase 4) allelss they possess and thus their likelihood of developing hereditary lymphoedema. Conditions associated with lymphoedema include Milroy-Nonne syndrome, which is early onset lymphoedema and lymphoedema praecox, which is late
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                                                                                                                        Human, gene therapy, lymphatic disorder; hereditary lymphedoema, Flt4, vascular endothalial growth factor receptor-3; VEGFR-3; VEGF-C; VEGF-D; fms-like tyrosine kinase 4; ss.
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Best Local Similarity 99.9%; Pred. No. 0;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 1, Applia Sequence 982, Appliance 4, Applia
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Sequence 7, Appli
Sequence 8, Appli
Sequence 25, Appli
Sequence 27, Appl
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Appl
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Sequence 6, Ap
Sequence 25, A
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Sequence 14, 7
                          Seguence 6, A
Seguence 25,
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US-08-99-811-1

Sequence 1, Application US/08999811

Sequence 1, Application US/08999811

Patent No. 5932540

APPLICANT: ROSEN, CRAIG A.

APPLICANT: ROSEN, CRAIG A.

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

TITLE OF SEQUENCES: 15

COUNTRY: MASHINGTON

STATE: DC

COUNTRY: USA

CINY: WASHINGTON

COUNTRY: USA

COMPTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

ADDION TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMP DC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/999,811

FLING DATE: HEREWITH

CLASSIFICATION NUMBER: US/08/999,811

FLING DATE: WENEWITH

FRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/550

FILING DATE: US/08/1994

PRIOR APPLICATION NUMBER: US/08/465,968

ATTORNEY/AGENT INFORMATION:

MAME: MARKONICZ, KAREN R.

REFERENCE/DOCKET NUMBER: 1488.1000004

TELEPRATION NUMBER: 36,351

REFERENCE/DOCKET NUMBER: 1488.1000004

TELEPRATION NUMBER: 36,351

REFERENCE/DOCKET NUMBER: 1488.1000004

TELEPRATION NUMBER: 12540

INFORMATION FOR SEQ ID NO: 1:

SEGUIENCE CHRACATERISTICS:

LENGTH: 1674 base pairs

TYPE: nucleic acid

STRANDENESS: double

TOWNORTHY TOWNORTS: Acid

STRANDENESS: double

TOWNORTHY TOWNORTS: Acid

STRANDENESS: double
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US-08-52430-6
US-08-58-895-25
US-08-58-895-25
US-08-601-132-25
US-08-611-132-25
US-08-611-132-25
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LOCATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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GENERAL INPORMATION:
APPLICANT: HU, UNG-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
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Best Local Similarity 100.0%;
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APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE

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                          121 GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAACACCCTTCTTTAAACCTCCATGTG 480
                                                     421 GTATAGATGTGGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
                                                                                                                                      481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGGCTGCAGTGCATGAACACCA
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NAME: ERIC K. STEFFE
REGISTATION NUMBER: 36,688
REGISTATION NUMBER: 1488.1000003/EKS
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEPHONE: (202)371-2640
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGHH: 1674 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
CLASSIFICATION:
                                                         FILING DALE.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
APPLICATION NUMBER: B-MAR-1994
CURRENT APPLICATION DATA:
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Best Local Similarity 100.
Matches 1674; Conservative
                                        APPLICATION NUMBER: US
FILING DATE: HEREWITH
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LOCATION: 12..80
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LOCATION:
FEATURE:
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; LOCATION;
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421 GTATAGATGTGGGGAAGGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG 480 	481 IGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGCTGCAGTGCATGAACACCA 540	541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCTCTCTCT	601 AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG 660 601 AACCAGTAACAATTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG 660	661 TTHCAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720	721 AGGCAGGAAGAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780	781 IGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840 	941 ATGACATCTGTGGACCAAACAAGAGCTGGATGAAGACCTGTCAGTGTGTCTGCAGAG 900 	901 CGGGGCTTCGGCCTGCCGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT 960 	961 GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCCAACGGAGAATTTGATGAAA 1020 	1021 ACACATGCCAGTGTATATGTAAAAAACTGCCCCAGAAATCAACCCTAAATCCTGGAA 1080	AGAAGTTCC 114 GAAGTTCC 114	SCCAGAAGGCTTGTGAGC 1	126	CTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT 13 	21 TGCCACAGTAGAACTGTCTGTGAACAGAGACCCTTGTGGGGTCCATGCTAACAAAAC 21 TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCTGTGCTAACAAAGAC	CATCTG 144	1441 CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCGATGACCAAACAGCCAAATTTCCTC 1500 1441 CAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCCAATGACCAAACAGCCAAAGATTTTCCTC 1500 1441 CAAAGGCCTCTTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAACAACAACATTTTCCTC 1500)))
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 TTCTGC 156	ATTCATITITATAGCAACAACAATIGGTAAAACTCACIGIGATCAATATITITAI 	1621 GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAA	T 3 -465-968-1 pence 1, Application US/08465968E	ent No. 6608182 IERAL INFORMATION: PPLICANT: Rosen et al. TLE OF INVENTION: Vascular Endothelial Growth Factor 2	LE REFERENCE: PF112P1 RRENT APPLICATION NUMBER: US/08/465,968E RERNT FILING DATE: 1995-06-06 RLIER APPLICATION NUMBER: 08/207,550	RLIER FILING DATE: 1994-03-08 MBER OF SEQ ID NOS: 10 FIWARE: Patentin Ver. 2.0	ENGTH: 1674 YPE: DNA KRANISM: Homo sapiens PBATURE:	AAME/KEY: CDS OCATION: (12)(1268) PATURE: AAME/KEY: sig peptide	OCATION: (12)(149) RAINE: RAND/KEY: mat_peptide OCATION: (150)(1268)	Score 1674; DB 4; Length 1674; Pred. No. 0;	ACTO	GGACTCG 1	ACTITICAGACACAGACACACACACACACACACACACATATACAACAAAAAATACAAAAAA	ACGACAGTTACCGTCTGTGTCCAGTGTACATCAAACTCATGACTTGTACTCTACCAGAAT 24	ATGGARAATGTRACAGTAGGARAAGGAAAGGGCGGCAACATAACAGAAACAG 30 ATTGGARAATGTRACAAGTAAGGAAAGGAAGGCGCAACATAACAGAAACAG 30 ATTGGAAAATGTRACAAGTCTRAGGAAAGGAAAGGAACATCAAAATAACAGAAAGG 30	301 CCAACCTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG 360 	AGATCTTGAAAAGTATTGATAATGAGAGAAAAGACTCAATGCATGC	

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B AGGACCAGTTACCGTCTGTGTCCAGTGTACATCAACTCATACTCTACCCAGAAT 240	151 AGATCTICABANGTATTGATAGAGGGGAAAGACTCAATGCATCCAGGGGGTGT 120 421 GATAGATCTICAAAAGTATTGATAGAGTGGAGAAAGACTCAATGCATCCACGGGAGGTGT 180 421 GATAGATCTICAAAAGTATTGATTAGAGTGGAGAAAAACTCCAATGCATCCACGGGAGGTGT 180 431 GATCGGTCTACAAATTGATTGAGTTGGAGACAAAAACTTCTTTAAACTTCAATGTGTG 180 431 TGTCGGTCTACAAATTGAGTTGGAGGTTGATTGAAATTACAAAACTTCATTAAACTTCAATGTG 180 431 TGTCGGTCTACAAATTGAGAGTTGTGAGTTGAAAAACTTCAATGAATTCAATGAATTCAATGAATTCAATTAAACTTCAATGAATTCAATTAAACTTCAATGAATTCAATTTAAACTTCAATGAATTCAATTTTAAAACTTCAATAACTTCAATGAATTCAATTTTAAAATTTCAAAAACTTCAATGAATTCAATTTTAAAAACTTCAATAACTTCAATGAATTCAATTTTAAAAAAAA
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	US GOGGENERAL INPORMATION: Sequence I Application US/08/06054A Sequence II Application US/08/06054A Sequence II Application US/08/06054A Sequence II Application US/08/06054A Sequence III Application US/08/06054A TITLE OF INVENTION: VARS-Related Protein NUMBER OF SEQUENCE ADDRESS: COMPUTER SHIPS SET SET SET SET SET SET SET SET SET SE

241 AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACT 241 ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGCTGGCAACATAA 241 ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGCTGGCAACATAA 301 CCAACCTCAACTCAAGGACAGAAGAACTATAAAATTTGGTGCAGCAGC 301 AGATCTTGAAAAGTATTGATAATGACTGTAAAAATTTGGTGCAGCAGCAGCAGCAGCAGCAGAAGAAGACTTTGAAAAAATTTGCTGCAGCAGCAGCAGCAGCAGCAGCAGAAGAAGAAGAATTTGGTGAAGAAGACTCAATGCATGC	#81 IGCCCTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA 90 #81 IGCCCGTCTACAGATGTGGGGGTTGTTTGAAATTACAGTGCCTGCTGTGAGTGCATGAACACCA 90 #81 IGCCGGGTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCT	1021 TITACAGCAAGTICATITICATIATAGACGTICCCTGCCAACACTACCAACAGTGTC 721 AGGCAGCGAACAAGACCTGCCCACCAATTACATGTGGAATAATCACATCTGCAGTGTC 721 AGGCAGCGAACAAGAACACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGTGACTCAACAAGATGGATTCC 781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGTGACTCAACAGATGGATTCC 781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGTGACTCAACAGATGGATTCC 781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGTGACTCAACAGATGGATTCC 781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGGAATGACTCAACAGATGGATTCC	841 ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAV 1201 ATGACATCTGGACCAACAAGGAGGTGGATGAAGAGACCTGTCAV 1201 ATGACATCTGGACCAACAAGAGGGTGGATGAAGAAGACTGGTCAA 901 CGGGGCTTCGGCCTGCCAACTGTGGACCCCACAAAGAACAACAAGA 901 GGGGCTTCGGCTGCCAGCTGTGGACCCCCACAAAGAACAAAGAAGAACAAGG 961 GTGCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGG 1321 GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGG	1021 ACACATCCAGTGTATGTAAAAGACCCCCAGAAATCAACCCCTAAATCTGGAA 144 1381 ACACATGCCAGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 144 1081 ACACATGCCAGTGTATGTAAAAGAACCTGCCCCAGAAATCCACCTGGAA 144 1081 AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAACTTCC 110 1141 ACCACCAAACATGTAAAGAAAGTCCACAGAAATGCTTGTTACAAAGGAAAGAATTCC 150 1141 ACCACCAAACATGCAGCTGTTAACAGAACGCCATGTACGAAAGAACTTCC 150 11501 ACCACCAAACATGTAAAGATGTGTGCGTTGTGTCCCTTCATAATGGCAAAGACCT 126 1261 CAGGATTTTCATAATAGTGAAGAATGTGTGTGTGTTGTTGTTGTAATTGGAAAAGACCAC 126 1261 AAATGAACTTAAAGATGAAGAAGTGTGTCGTTGTTGTCCTTCATAATGGAAAAACTGTGT 132 1261 AAATGAACTAAAGATTGTAACTGTTTTTCAATTTTTTAATTGGAAAAACTGTGT 132 1261 AAATGAACTAAAATTGTAATTTTCCAGTTTCATTTTTTATTGGAAAAACTGTGT 136 1621 AAATGAAGATTGTACTGTTTTTCCAGTTTCTATTATGGAAAAACTGTGT 168 1621 AAATGAAGATTGTACTGTTTTTCCAGTTTCTATTATGGAAAAACTGTGT 168
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech)

CURRENT APPLICATION DATA:

FILING DATE: 30-Aug-1996

CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, James Wood, William I. TITLE OF INVENTION: VEGF-Related Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: P-40,378
REPREMOKED FOOGRET NUMBER: P0963R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/003491
FILING DATE: 08-Sep-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08706054A Patent No. 6451764 GENERAL INFORMATION:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity
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US-09-313-299-2
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Patent No. 657660B
CENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE CO INVENTION: VEGF-RELATED PROTEIN
FILE REFERENCE: P0965R1DI
CURRENT FILING DATE: 1999-08-17
EARLIER FILING DATE: 1996-08-30
BARLIER APPLICATION NUMBER: US 60/003,491
BARLIER FILING DATE: 1996-08-30
BARLIER FILING DATE: 1996-08-30
MUMBER OF SEQ ID NOS: 12
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Pred. No. 0;
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                                      TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INPORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1674 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
                 TELECOMMUNICATION INFORMATION
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TITLE OF INVENTION: Human Vascular EndothelialGrowth Factor
WUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CACCLI, STEWRAT & OLSTEIN
STREET: 6 BECKER FARM ROAD
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COUNTRY: NOSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER: DAN PS. S. SINCH DISKETTE
COMPUTER: LIBM PS. S. SINCH DISKETTE
COMPUTER: LIBM PS. S. SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09001
FILING DATE: G. JUN SS
PRICATION NUMBER: 08/465,968
FILING DATE: G. JUN SS
PRICATION NUMBER: 08/465,968
FILING DATE: G. JUN SS
APPLICATION NUMBER: 08/465,968
FILING DATE: G. JUN SS
APPLICATION NUMBER: 08/465,968
FILING DATE: B. MAR 1994
ATTORNARY AGENT INFORMATION:
AMAINEY AGENT INFORMATION:
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-288
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION DATE:
PRIOR APPLICATION NUMBER: PCT/F196/00427
APPLICATION NUMBER: PCT/F196/00427
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATE: 28-JUN-1996
PRIOR APPLICATION DATE: 28-JUN-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 12-JAN-1996
PRIOR APPLICATION NUMBER: 08/601,132
FILING DATE: 12-JAN-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133

FILING DATE: 01-AUG-1995

PRIOR APPLICATION NUMBER: 08/340,011

APPLICATION NUMBER: 08/340,011

APPLICATION NUMBER: 38/153

RAFERROCK DAVIG A.
RAGISTRATON NUMBER: 38/153

REGISTRATON NUMBER: 38/153

REFERROCK/DOCKET NUMBER: 28/967/33

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 13/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
  COMPUTER READABLE FORM:
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STRANDEDNESS:
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; LOCATION:
US-08-795-430-7
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1653; Conservative 0
CDS
352..1608
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APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun

; Sequence 7, Application US/08795430; Patent No. 6130071; GENERAL INFORMATION:

3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive

STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402

Db 1481 ACCACCAAACATGCAGCTGTTACAGACGCCATGTACGAACGCCACAAAGACCAC 1540 1201 CAGGATTTTCATATAGTGAACATGTGTCGTTGTGTCCCTTCATATTGCCAAAGACCAC 1600 1541 CAGGATTTTCATATAGTGAACATGTGTTCTTTGTCCTTCATATTGCAAAAGACCAC 1600 Qy 1261 AAATGAGCTACAGATTTTCCAGTTCTTCATTTTTTTTTT	WESULT 11 WE OB-155-700-7 WE OB-155-700-7 Sequence 7, Application US/09355700 Patent NO. 651946 Patent NO. 651946 Alitalo, Marit Us. conity Alitalo, Marit Us. conity Alitalo, Marit Us. conity Joukov, Vladimir Us. conity Frotein and Gene, Mutants Thereof, and Uses Thereof NUMBER OF SEQUENCES: 59 CORRESPONDENCE 159 CORRESPONDENCE 1500 Gears Tower, 233 South Wacker Drive CITY: Chicage 1101001 STREET: 6100 Gears Tower, 233 South Wacker Drive CONTRY: United States of America STATE: Illinois CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: Object 1000 CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: Object 1000 CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: United States of America CONTRY: Object 1000 CONTRY: United States of America CONTRY: Unit
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                                                                                      NAME: Gass, David A.

NAME: Gass, David A.

REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1997 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

98.7%; Score 1651.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1653; Conservative 0; Mismatches
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-11995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
LOCATION: 352..1608
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-355-700-7
                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: 41
CORRESPONDENCE ADDRESS: 41
CORRESPONDENCE ADDRESS: ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
SITE: Chicago
SIATE: Illinois
COUNTRY: United States of America
ZIF: G606-6402
CONDUTRY: United States of America
ZIF: G606-6402
COMPUTRY: Lininois
COMPUTRY: Lininois
COMPUTRY: Law PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,132
FILING DATE:
CLASSIFICATION NUMBER: 28113/33118
REFERENCE/ORCKET NUMBER: 28113/33118
TELECPHONE: 312/474-6300
TELEPRAX: 25-3856
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1997 base pairs
TYPE: nucleic acid
STAPES: Lininois
TYPE: nucleic acid
STAPES SINGLES: Single
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Pred. No. 0;
0; Mismatches
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Similarity 99.9%;
33; Conservative
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658..1608
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LOCATION:
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US-08-601-132-32
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Best Local Simi
Matches 1653;
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Qy 1 GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGCTCGCCGC	521 AGAGCAGTTACGGTCTGTGTCCAGTGTACATGAACTCATGACTGTACTCTT 241 ATTGGAAAATGTACAAGTGTCCCAGGTAAGGAAAGGAGGCTGGCAACATAACAC 581 ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAC 301 CCAACCTCAAGTGTACAAGGACAGAAGGAAGGAGGCTGGCAACATAACAC 641 CCAACCTCAACTCAAGGACAGAAGAAGACTATAAAATTTGGTGCAGCACATTR 641 CCAACCTCAAAGTATTGATAAATGAGGAAGACTATAAAATTTGGTGCAGCACATTR 641 CCAACCTTGAAAAGTATTGATAATGAGGAAGACTATAAAATTTGGTGCAGCACATTR 661 CCAACCTTGAAAAGTATTGATAATGAGGGAGAAGATTGCTGCAGCACCCCACG	GTATAGATGTGGGGAAGGGTTTGGAGTGGGGACAAACACCTTTTAAACCTCCATGTG GTATAGATGTGGGGAAGGGGTTTGGAGTTTGGACACACCACTTTTAAACCTCCATGTG GTATAGATGTGGGGAAGGGTTTGGAGTTTGGAGACACCTTTTTAAACCTCCATGTG TGTCCGTCTACAGGTGTGGGGGGTTGCTGCAATAGTGAGGGGCTGCATGAACACGTGATGAACACCT TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCCA TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCCA GCACGAAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCT	OY 601 AACCAGTAACAATCTTTGCCAATCACATTCTGGCGATGCATGTTAAACTGGATG 660 Db 941 AACCAGTAACAATCAGTTTTGCCAATCACATGCTGCTTAAACTGGATG 1000 OY 661 TITACAGACAAGTTCATTCATTATAGACGTTCCTGCCGGCAACATGTCTAAACTGGATG 1000 OY 1001 TITACAGACAAGTTCATTCATTATAGACGTTCCTGCCAGCAACATGTC 720 Db 1001 TITACAGACAAGATCATTCATTATAGACGTTCCTGCCAGCAACACACATGTC 1060 OY 721 AGGCAGCAACAAGACCTGCCCCACAATTACATGTGGAATAATCACATCTGCAGATGC 780 Db 1061 AGGCAGCGAACAAGACTTCATTATAGATTAGATGGAATAATCACATTGCAGATGC 1120 OY 781 TGGCTCAGGAACAAGACTTTATATTTTACATTAGATTACATGAAATGAATTCC 840 Db 1121 TGGCTCAGGAAGATTTTATGTTTTCCTGGAAGACTCAACAAGATGGATTCC 1180	841 1181 901 1241 961 1301 1021 1361
	RESULT 13 US-08-671-573B-32 Sequence 32, Application US/08671573B Settle No. 6645933 Settle No. 6645933 Fatent No. 6645933 TITLE OF INVENTION: Receptor Ligand TITLE OF INVENTION: Receptor Ligand NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun	CITY: Chicago States fores, 239 South market Live CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: Flower Flower Compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBLE COMPATE: Parentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/671,573B FILING DATE: 28-UM-1996 CLASSIFICATION: 415	PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/601,132 FILING DATE: 14-FEB-1996 PRIOR APPLICATION NUMBER: 08/585,895 FILING DATE: 12-JAN-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/510,133 FILING DATE: 01-AGG-1995 ATTORNEY AGENT INFORMATION: NAME: Gass, David A. REGISTRATION NUMBER: 38,153 REPRECEMENCE/DOCKET NUMBER: 28967/33348 TELECOMMUNICATION NUMBER: 28967/33348 TELECOMMUNICATION NUMBER: 28967/33348	TELEX.: 25-386 TELEX.: 25-386 INPORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 1997 base pairs TYPE: nucleic acid STRANDENESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA FATURE: NAME/KEY: CDS LOCATION: 352.1608 US-08-671-5738-32 Query Match Best Local Similarity 99.7%; Score 1651.8; DB 4; Length 1997; Best Local Similarity 99.9%; Mismatches 2; Indels 0; Gaps 0;

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TTACATETGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36.351

REFERENCE/DOCKET NUMBER: 1488.1000004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371.2540

TELEPHONE: (202)371.2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 15.26 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE: TYPE: CDNA

FEATURE:
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143..1120
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71..142
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Best Local Similarity
Matches 1526; Conserv
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LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
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US-08-999-811-3
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Parent No. 5932540
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CRO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX
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CITY: WASHINGTON
STREET: 1100 NEW YORK AVENUE
COUNTRY: USA
ZIP: 20065
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/207,550
FILING DATE: 08-MAR-1994
FILING DATE: 06-JUN-1995:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

RELICATION NUMBER: US/09/042,105

FILING DATE: HEREWITH
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Pred. No. 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
CLASSIFICATION:
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APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
CLASSIFICATION:
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APPLICATION NUMBER: TO BE ASSIGNED BY STANDARD BATE: TO BE ASSIGNED BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDARD BY STANDAR
STREET: 1100 NEW YORK AVENUE CITY: WASHINGTON
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91.2%; Sco
Best Local Similarity 100.0%; P:
Matches 1526; Conservative 0;
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US-09-042-105-3
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           GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
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Patent No. 6040157
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CRO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
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Qy Dp	989 CCARIGIGGGGCCAACCGAGAAITIGAIGAAAACACAIGCCAGIGIGIAIGIAAAAGAAC 1048 			
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75 25 29	1109 ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG 1168 			
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λ 20 20	1289 GITCARCGAITITCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGT			
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y da	1469 CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAAGAATGACTATA 1528			
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100.0%; Score 1674;
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1: /cgn2_6/ptodata/1/pubpna/DS7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PST_MSW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/DS6_NEW_PUB.seq:*

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9 175.8 10.5 328 9 US	09-795-006A-168	168
0 174.2 10.4 397 9 US	09-795-006A-110	110
1 173.2 10.3 394 9 US	09-795-006A-78	78,
2 169.4 10.1 397 9 US	09-795-006A-104	104
3 168.4 10.1 394 9 US	09-795-006A-72	72,
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INFORMATION:		
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Sequence 7, A Sequence 23, Sequence 3, A

QY 1321 TGCCACAGTAGAACTGTCTGTGAACAGAGACCCTTGTGGGTCCATGCTAACAAGACA 1380 DD 1321 TGCCACAGTAGAACTGTCTGTGAACAGAGACCCTTGTGGGTCCATGCTAACAAAGACA 1380 QY 1381 AAAGTCTGTCTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG 1440 DD 1381 AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG 1440 DD 1441 CAAAAGGCCTCTTGTAAAGACTGTTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC 1500 DD 1441 CAAAAGGCCTCTTGTAAAGAATGACTATTTTTTTTTTTT	RESULT 3 US-10-127-551-1 Sequence 1, Application US/10127551 Sequence 1, Application US/10127551 Publication No. US2020120123A1 GENERAL INFORMATION: APPLICATION WORDER: FILE REFERENCE: PF112P1 CURRENT PAPLICATION NUMBER: US/10/127,551 FILE REFERENCE: PF112P1 CURRENT PAPLICATION NUMBER: EAALIER PEPLICATION NUMBER: 08/465,968 PRIOR APPLICATION NUMBER: EAALIER APPLICATION NUMBER: 08/207,550 PRIOR APPLICATION NUMBER: EAALIER APPLICATION NUMBER: 08/207,550 PRIOR APPLICATION NUMBER: EAALIER APPLICATION NUMBER: 08/207,550 PRIOR APPLICATION NUMBER: EAALIER APPLICATION NUMBER: 08/207,550 NUMBER OF SEQ ID NOS: 10 SEQ ID NO 1 LENGTH: 16*4 SEATURE: NUMBER OF SEQ ID NOS: 10 SEATURE: NAME/KEY: CDS LOCATION: (12) (1268) FEATURE: NAME/KEY: mat peptide LOCATION: (12) (1268) FEATURE: NAME/KEY: mat peptide LOCATION: (12) (1268)	Query Match 100.0%; Score 1674; DB 13; Length 1674; Best Local Similarity 100.0%; Pred. No. 0; Matches 1674; O; Gaps 0; Astches 1674; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GTCCTTCCACCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGGCGCTG 60 Qy 61 CGCTGCTCCGGGGTCCTCGGGGGCCCGCCGCCGCCGCCGC
181	AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG TTTACAGACAAGTTCATTCCATTATTAGACGTTCCTGCCGATGCATGTCTAAACTGGATG TTTACAGACAAGACCTTCCATTATTAGACGTTCCCTGCCGACACACTTACCACGGATG AGCAGCGAACAAGACCTGCCCCACCATTTACATGTGGAATAATCACATTCTGCAGTGTC AGCAGCGAACAAGACCTGCCCCACCATTTACATGTGGAATAATCACATTCTGCAGTGTC AGCAGCGAACAAGACCTGCCCCACCATTTACATGTGGAATAATCACATTCTGCAGTGCT AGCACCAGAACAAGACCTGCCCCACCAATTACATTGTGGAATAATCACAATTCTGCAGTGCT AGCACCAGAACAAGACCTGCCCACCAATTACATTGTGGAATAATCACAACACACAC	AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAATTCC AACACCAAACATGCATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC ACCACCAAACATGCAGCTGTTACAGAAAGTCCATGTACGAACGCCAGAAGAGTTCC ACCACCAAACATGCAGCTGTTACAGACGCCATGTACGAACGCCAGAAGGCTTGTGAGC ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACGCTTGTATTGGCAAAGACCAC CAGGATTTTCATATAGTGAAGAAGTGTGTGTGTGTCCCTTCATATGGCAAAGACCAC CAGGATTTTCATATAGTGAAGAAGTGTGTGTGTGTGTCCCTTCATATTGGCAAAAGACCAC AAATGAGCTAAGATGTACTGTTTTCCAGTTCATCTATTTTTATTGGCAAAACTGTGT AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATTTCTATTATGGCAAAACTGTGT AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATTCTATTATGGAAAACTGTGT AAATGAGCTAAGATTGTACTGTTTTTCCAGTTCTATTTCTATTATGGAAAACTGTGT AAATGAGCTAAAGATGTACTGTTTTTCCAGTTCTATTTCTATTATGGAAAACTGTGT AAATGAGCTAAAGATGTACTGTTTTTCCAGTTCTATTTTTTTT

Db 1261 AAAIGAGCTAAGATTGTACTGTTCATCGATTTCTATTATGGAAAACTGTGT 1320 Qy 1321 TGCCACAGTAGAACTGTCTGTGAACAGAGACCCTTGTGGGTCCATGCTAACAACACA 1380 Db 1321 TGCCACAGTAGAACTGTCTGTGAACAGACACCCTTGTGGGTCCATGCTAACAACACAC 1380 Qy 1381 AAAGTCGTCTTTCCTGAACAGACAGACCCTTGTGGGTCCATGCTAACAACACACA 1380 Qy 1441 CAAAAGGCCTCTTTCCTGAACACATGGATAACTTTACAGAAATGGACTCATCTG 1440 Qy 1441 CAAAAGGCCTCTTTCTGAACACCATGGATAACTTTACAGAAATGGACTCATCTG 1440 Db 1501 TGGATTTCTTTAAAAGAACTGGTTTTCTGCCAAACAGCCAAGATTTTCCTC 1500 Qy 1501 TGGATTTCTTTAAAAGAATGACTATATAATTTACACAAAAAATTGTTTCTC 1500 Qy 1501 TGGATTTCTTTAAAAGAATGACTATATAATTTACCACTAAAAATTGTTTCTGC 1500 Qy 1501 TGGATTTCTTTAAAAGAATGACTATATAATTTACCACTAAAAATTTTTTCTTCTC 1500 Qy 1501 TGGATTTCTTTAAAAGAATGACTATATAATTTTTCCACTAAAAATTTTTTTT	RESULT 4 US-10-084-488-1 Sequence 1, Application US/10084488 Publication No. US20030028007A1 Publication No. US20030028007A1 TITLE OF INVENTION: APPLICANT: Human Genome Sciences, Inc. ITILE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2 NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STREET: 9410 KEY WEST AVENUE COUNTRY: USA ZIP: 20850 COMPUTER: BEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible CORPUTER: IBM PC Compatible COMPUTER: BEADABLE PCDS/MS-DOS SOFTWARE: PREFAING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/10/084,488 FILING DATE: 28-Feb-2002 CLASSIFICATION: UNKNOWN PRIOR APPLICATION DATA: APPLICATION NUMBER: US/09/623,725 FILING DATE: 07-8ep-2000 FILING DATE: 13-MAR-1998 APPLICATION NUMBER: US 09/107,997 FILING DATE: 30-UJN-1998 ATTORNEY/AGBWT INPORMATION: NAME: MICHELE M. WALES REGISTRATION NUMBER: 43,975 REGISTRATION NUMBER: 43,975 REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFAX: (301)309-8504 TELEFAX: (301)309-8504 TELEFAX: (301)309-8439 INPORMATION FOR SEQ ID NO: 1. SEQUENCE CHARACTERISTICS: LENGTH: 1674 base pairs TYPE: MULCleic acid TYPE: GONA.
181		GGGGGCTTCGGACCCACCACAAAGACTAGACAGAACTCATGCCGGT GGGGGCTTCGGACCCACCCACAAAGACTAGACAGAACTCATGCCGGT GTGTCTGTAAAAACAACTCTTCCCCAGCCCATGGGGGCCAACCGAGAATTTGATGAAA ACACATGCCAGTGTGTATGTAAAAGAACTGCCCAGAAATTTGATGAAA ACACATGCCAGTGTATGTAAAAGAACTGCCCCAGAAATCACCCTAAATCCTGGAA ACACATGCCAGTGTATGTAAAAGAACTGCCCCAGAAATCACCCTAAATCCTGGAA AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGATTCC ACACACACACATGCAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGATTCC ACACACACACACACACACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGATTCC ACCACAACATCACACTTACAGACGCCATTCTTAAAAGGAAAGCTTGTGAGC ACCACAACATCACACTTACAGACGCCATTCTTCTTATTGGCAAAAACTGACCC CAGGATTTTCATAAAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCCC CAGGATTTTCATAAAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC AAATGAGCTAAAATGTTACAAAGAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC AAATGAGCTAAAATGTTACAAAAAGTGTTCTTCTTATTTGGCAAAAACTGTGTGT AAATGAGCTAAAATGTTACCAATTTCCTATATTGGCAAAAACTGTGTT AAATGAGCTAAAAATGTTACCAGTTCTTCTATATTGGCAAAAACTGTGTT AAATGAGCTAAAAATGTTACCAGTTCTTATTTCTATATTGGCAAAAACTGTGTTTATTCTATATTGGCAAAAACTGTTGTTATTCTTATTTCTATATTGCCAAAAACTGTTTTTCTTATTTGCAAAAACTGTTTTTCTTATTTTCTTATTTTCTATATTTTCTTATTTTTT

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              ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGAGCCTGTCAGTGTGTCTGCAGAG
                                                                    GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCCAACCGAGAATTTGATGAAA
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                                                CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAAGAACTAGACAGAAACTCATGCCAGT
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US-10-120-398-1
; Sequence 1, Application US/10120398
; Sequence 1, Application US/10120398
; Publication No. US20030170786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENION: Vascular Endothelial Growth Factor-2; FILE REFERENCE: PF112P7
; CURRENT APPLICATION NUMBER: US/10/120,398
; CURRENT FILING DATE: 2002-04-12; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 71
; NUMBER OF SEQ ID NOS: 71
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SEQ ID NO 1
LENGTH: 1674
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100.0%; Score 1674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1674; Conservative 0; Mismatches
                                                                                                                  NAME/KEY: CDS
LOCATION: 12..1268
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                 sig_peptide
12..80
                                                                mat peptide
81..1268
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LOCATION:
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PRGANISM: Homo sapiens FRATURE: NAME/KEY: sig_peptide LOCATION: (12)(80) OTHER INFORMATION: FEATURE: NAME/KEY: CDS LOCATION: (12)(1268) COTHER INFORMATION: FEATURE: NAME/KEY: MALE peptide LOCATION: (81)() COTHER INFORMATION: COTHER INFORMAT		121 ACCTCTCGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	QY 241 ATTGGAAAATGTACAAGTAAGGAAAGGAGGCTGGCAACATAACAGAAACAGG 300 DD 241 ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAAAAAGG 300 QY 301 CCAACCTCAACTCAAGGACACTATAAAATTTGCTGCAGCACATTATAATACAG 360 DD 301 CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG 360	QY 361 AGATCTTGAAAAGTATTGATAATGAGTGGAGAAGACTCAATGCATGC	QY 481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGCTGCAGTGCATGAACACCA 540 Db 481 TGTCCGTCTACAGATGTGGGGTTGCTGCAATAGTGAGGGCTGCAGTGCATGCA	QY 601 AACCAGTAACAATCAGTTTTGCCAATCACTTCCTGCCGATGCATGTCTAAACTGGATG 660 Db 601 AACCAGTAACAATCAGTTTTGCCCAATCACTTCCTGCCGATGTCTAAACTGGATG 660 QY 661 TTTACAGACAAGTTCCATTATTACACGTTCCTGCCAGCAACACACAC	OY 721 AGGCAGCGAACAGACCTGCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780 DD 721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC 780 OY 781 TGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGAGAATGACTCAACAGATGGATTCC 840.

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TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REFERENCE: PF112P8
CURRENT APPLICATION NUMBER: US/10/120,377
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GENERAL INFORMATION:
APPLICANT: Rosen, Craig, et al.
TITE OF INVENTION: Vascular Endotl
FILE REFERENCE: PF112P8
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SOFTWARE: Patentin version 3.1
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                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig peptide
LOCATION: (12)...(80)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CDS
LOCATION: (12)...(1268)
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NAME/KEY: mat_peptide

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OTHER INFORMATION:
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Sequence 1, Application US/10346802
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CURRENT FILING DATE: 2002-04-12
PRIOR PAPLICATION NUMBER: 60/283,391
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PACENTIN VERSION 3.1
LENGTH: 1674
TYPE: DNA
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TYPE: NAME/KEY: sig_peptide
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FRATURE:
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                      APPLICANT: Lee, James
APPLICANT: Lee, James
TITLE OF INVENTION: VEGF-RELATED PROTEIN
CURRENT WOOD, WAILiam I.
CURRENT APPLICATION NUMBER: US/10/346,802
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US/09/313,299B
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/09
PRIOR FILING DATE: BARLIER FILING DATE: 1996-08-30
PRIOR FILING DATE: BARLIER FILING DATE: 1995-09-08
NUMBER OF SEQ ID NOS: 12
LENGTH: 2031
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Pred. No. 0;
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Best Local Similarity 99.8%;
Matches 1667; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY: Human
; LOCATION: 1-2031
; OTHER INFORMATION:
US-10-346-802-1
     GENERAL INFORMATION
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US-10-346-802-2/c
| Sequence 2, Application US/10346802 |
| Publication No. US20030166873A1 |
| GENERAL INFORMATION: |
| APPLICANT: Lee, James |
| APPLICANT: Wood, William I: |
| TITLE OF INVENTION: VEGF-RELATED PROTEIN
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NAME/KEY: misc feature

CTHER INFORMATION: Incyte ID No. US20030119009A1 550425CB1

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                                                                     ACTIVATION
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APPLICANT: Susan Stuart
APPLICANT: Jed G. Nuchtern
APPLICANT: Jed G. Nuchtern
APPLICANT: Sharon E. Plon
APPLICANT: Sharon E. Plon
TITLE OF INVENTION: GENES REGULATED BY MYCN ACT
TITLE REFERENCE: PA-0046 US
CURENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR PLING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SQFTWARE: PERL Program
SGTWARE: PERL Program
LENTH: 1786
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Best Local Similarity 99.7
Matches 1667; Conservative
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ORGANISM: Homo sapiens
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FILE REFERENCE: P0963R1D1

CURRENT APPLICATION NUMBER: US/10/346,802

CURRENT FILING DATE: 2003-01-17

PRIOR APPLICATION NUMBER: US/09/313,299B

PRIOR FILING DATE: 1990-05-17

PRIOR FILING DATE: 1990-05-17

PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-30

PRIOR FILING DATE: EARLIER FILING DATE: 1995-09-08

PRIOR FILING DATE: EARLIER FILING DATE: 1995-09-08

NUMBER OF SEQ ID NOS: 12

LENGTH: 2031

TYPE: DNA

ORGANISM: Human

PEATURE:
NAME/KEY: Human

LOCATION: 1-2031

LOCATION: 1-2031
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Pred. No. 0;
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US-10-346-802-2
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Best Local Similarity 99.7%;
Matches 1666; Conservative
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Patent No. US20020151680A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAG AND PROTEINS
FILE REFERENCE: 28967/35977B

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| PUBLICATION NO. US20030026759A1
| GENERAL INFORMATION:
| APPLICANT: Ferrell, Robert E. |
| APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: First APPLICANT: FIRST APPLICANT: FIRST APPLICANT: FIRST FIRST APPLICANT: FIRST FIRST FIRST APPLICANT: THE FIRST RECEPTOR TYROSINE KINASE (VEGFF-3)
| FILE REFERENCE: 28967/35255A
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT FILING DATE: 2001-02-26
FRIOR APPLICATION NUMBER: US 60/205,331
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/185,205
FRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 1997
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Best Local Similarity 99.9
Matches 1653; Conservative
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; NAME/KEY: CDS
; LOCATION: (352)..(1608)
US-09-795-006A-21
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ORGANISM: Homo sapiens
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US-10-201-386-7
Sequence 7, Application US/10201386
Publication No. US20030091567A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C)
TITLE OF INVENTION: AND GENE, MUTANITS THEREOF, AND USES THEREOF
FILE REPRENCE: 25967/34140A
CURRENT APPLICATION NUMBER: US/10/201,386
GURRENT FILING DATE: 2002-07-23
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CURRENT APPLICATION NUMBER: US/09/375,248
CURRENT FILING DATE: 1999-08-16
EARLIER APPLICATION NUMBER: PCT/US99/06133
EARLIER APPLICATION NUMBER: PCT/US99/06133
SEQ ID NOS: 28
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
LYPE: DATA
CONTAIN: 1997
TYPE: DATA
CORANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (352)..(1611)
FRATURE:
COTHER INFORMATION: Human CDNA for prepro-VEGF-C
US-09-375-248-3
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                                                                                                                                                                                                                                                                              Query Match
98.7%; Score 1651.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1653; Conservative 0; Mismatches
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98.7%; Score 1651.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1653; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US/09/534,376
PRIOR FILING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR APPLICATION WUMBER: 00/355,700
PRIOR APLICATION NUMBER: PCT/US98/01973
PRIOR PLING DATE: 1996-020
PRIOR PLING DATE: 1996-020
PRIOR PLING DATE: 1997-02-05
PRIOR PLING DATE: 1996-02-15
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LOCATION: (352)..(1608)
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US-10-201-386-7
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                                                                            Sequence 23, Application US/10262538
Publication No. US20030113324A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
FILE REPERENCE: 28967/37564
CURRENT APPLICATION NUMBER: US/10/262,538
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Version 3.0
LENGTH: 1997
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APPLICANT: De Vries, Gerald W.
TITLE OF INVENTION: Methods of Extending Corneal Graft
TITLE OF INVENTION: Survival
FILE REFERENCE: P-AR 4951
CURRENT APPLICATION NUMBER: US/10/081,126
CURRENT FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                      DB 14;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                   98.7%;
larity 99.9%;
Conservative (
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) LOCATION: (372)...(1628)
US-10-081-126-3
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Simi
Matches 1653;
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Database :

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AM9195617 xn844911.x
AA923193 om48601.s
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BW070215 xa03c10.x
BW070215 xa03c10.x
BW070215 xa03c10.x
BW050633 UI-H-FU1-
BE218812 hv45a10.x
CB854820 UI-H-FU1-
BW15186 ie95f08.x
AW341345 xz98f10.x
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BW054973 ie952b06.x
BR113454 BX113454
BR13454 BX113454
BR137929 wf34911.x
BW558208 601644672
BM137929 wf34911.x
AM459340 tj96h12.x
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BW310008 HW95925
AW3713 yyl5b12.s1
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AW3772 AGENCOURT
BW3173 yyl5d12.s1
BW31700 yyl5d12.s1
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BW31775 AGENCOURT
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A1066424 oz84h10.x
B1154009 602871066
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
     CA421508
CCA421508
AW195617
AA923193
AW070215
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BC199911
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AA1545486
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AK047844.1 GI:26339001
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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448.6
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AUTHORS
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                          Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Mishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Kazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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/db_xref="GI:26339002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research (Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, 230-0045, Japan (E-mail:genome-reseggsc:riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev gage="16 days embryo"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 kull-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2450)
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vascular endothelial growth factor C (MGD|MGI:109124,
GB|NM_009506, evidence: BLASTN, 99%, match=1784)"
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/
URL:http://dantom.gsc.riken.go.jp/.
Location/Qualifiers

1 . 2450
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/ mol_type="mRNA"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0605 row: g column: 22
High quality sequence stop: 806.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

National topos.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.
    CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAGAACTAGACAGAACTCATGCCAGT
                                        GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
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CA488579 858 bp mRNA linear EST 14-NOV-2002 AGENCOURT 10808789 MAPcL Homo sapiens cDNA clone IMAGE:6720351 5', mRNA sequence.
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1 (bases 1 to 858)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CCTTCGAGTCCGGACTCGACCTCTCGGACGCGGACGCGACGCGGGGCGACGCGGGCCTT
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E. (Bases I to 831)

S. (Bases I to 831)

I. (Bases I to 831)

D. National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Library Preparation: Consortium/Library Preparation: Consortium/Library Preparation: Consortium/Library Preparation: Library Preparation: Library Preparation: Library Preparation: Library Column: 04

High quality sequence stop: 810.
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/lab host="DH10B (T1 phage-resistant)"
/clone lib="NOI CGAP Skn4"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                               CTGTGTTGCCCCCAGTAGAACTGTCTTGTGAACAGAGGAGACCTTGTGCGTCCATGCTAAC
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                                                                                                                                                                                                      781 AAAGACAAAAGTCTGTCTTTCCTGAACCAATGTGGATTACTTTACAGAACATGGACCTGG
                                                                                                                                                                                                                                                                                                                    841 AGCICAICIGCAAAAGGCCICIIGIAAAGACGGTITICIIGCCAIIGACCAAAAAGCCC
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Pred. No. 2.5e-118;
0; Mismatches 1; Indels 4;
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llarity 99.4%;
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/tissue_type="Enclored"
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/dev_stage="Adult"
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/lab_host="Pullub"
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/clone lib="NCI CGAP_EN12"
/note="Corgan: Bone; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI CGAP_EN12 is a cDNA library containing the following tissue(s): Enchordroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library is CCGGTCACTC. The cell lines was provided by Dr James Marthi from University of Iowa.

TAG_IIB=U1.H-FG0

TAG_LIB=U1.H-FG0

TAG_ENESUR=Enchondroma cell line (Mix of ENI and EN2)
TAG_ENESUR=Enchondroma cell line (Mix of ENI and EN2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, Dento-soares@uliowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-53, APT rich#Low_complexity (matched compliment)
BOLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA421508
UI-H-FGG0-bcu-e-12-0-UI.sl NCI CGAP ENI 2 Homo sapiens cDNA clone
UI-H-FGG0-bcu-e-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                        721 CAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGAACG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bumanlai, Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 750)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Gancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                      1110 CAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAG-ACG
                                                                                                                 661 TGCCCCAGAATCAACCCCTANATCCTGGAAATGTGCCTGTGAATGTACAGAAAGTCCA
                                                                                                                                                                                                                                                                                                                                 1209
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                                                                                                                                                                                                                                                                                                                          1169 GCCATGTACG-AACCGCCAGAAGGC--TTGTGAGCCAGGATTTT
                                                                                                                                                                                                                                                                                                                                                                                    GCCATGTACGAAACCGCCAGAAAGCCTTTGTGAGCCANGAATTT
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|mol_type="mkNA"
|db xref="taxon:9606"
|clone="UI-H-FG0-bcu-e-12-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .750
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CA421508.1 GI:24784163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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Unpublished (1997)
                                                   1050
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CA421508/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                                                                                                  Lorganism="Homo sapiens"

| Organism="Homo sapiens"
| Organism="MRNA"
| Mol_Lype="MRNA"
| Mol_Lype="MRNA"
| Abol="Emaxon:9606"
| Olone="InhoE":6720351"
| Cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
| Abost="BYDHIDB"
| Alb host="BYDHIDB"
| Alb host="MNAPC"
| Abost="MAPC"
| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAAT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TACAIGIGGAATAATCACATCIGCAGAIGCCIGGCICAGGAAGATTITAIGITITICCTCG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/DLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMM4279 row: I column: 15
Plate: LLAMM4279 row: I column: 15
Plate: Location/Qualifiers
Location/Qualifiers
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99.0%; Pred. No. 4.6e-118;
live 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 816; Conserv
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/mol type="mono" sapiens
/mol type="mono" sapiens
/db xref="taxon:966"
/clone="UI-FH0-bco-p-03-0-UI"
/tissue type="Human Chondrosarcoma Cell Line"
/dev stage="Adult"
/dev stage="Adult"
/dev stage="Adult"
/dev stage="Adult"
/dev stage="Adult"
/dore="Organ: Bone; Vector: pr773-Pac (Pharmacia) with a modified polylinker; Site 1: Ecok I; Site 2: Not I;
/clone lib="NoI GABP FH0"
/mote="Organ: Bone; Vector: pr773-Pac (Pharmacia) with a modified polylinker; Site 1: Ecok I; Site 2: Not I;
/note="Organ: Bone; Vector: pr773-Pac (Pharmacia) with a modified polylinker; Site 1: Ecok I; Site 2: Not I;
/note="Organ: Bone Acade I Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an Ecok I adaptor, digested with Not I, and cloned directionally into pr773-Pac vector. The oligomuclecide used to prime the synthesis of first-strand CDNA contains a library tag sequence that is located between the Not I site and the (dT) 8 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr James Martin from University of Icom
                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-51, AAT rich#Low_complexity (matched compliment)
POLYA=Yes.
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TISSUE-Human Chondrosarcoma Cell Line CS8 - Grade 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1045 GAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAAATGTACAGAAA
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.larity 99.2%; Pred. No. 1.1e-109;
Conservative 0; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                      1. .748
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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TAG_SEQ=AGAATCCGGC"
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Matches 743; Conserv
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     JOURNAL
COMMENT
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Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 498.

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 CTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGGATTTTCCTCTTGTGATTTTC
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omd4800.1s1 Soares NFL T GBC S1 Homo sapiens CDNA clone
IMAGE.1544257 3' similar to SW:VEGC HUMAN P49767 VASCULAR
ENDOTHELIAL GROWTH FACTOR C PRECURSOR ;, mRNA sequence.
                                                4,
                                                Indels
      Length
                                                41;
Score 702; DB 10;
Pred. No. 3.7e-105;
0; Mismatches 41;
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  Query Match
Best Local Similarity 94.4%;
Matches 760; Conservative
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Homo sapiens
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AA923193/c
LOCUS
DEFINITION
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VERSION
XEYWORDS
SOURCE
ORGANISM
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/UDD type="mRNA"
// Aref="taxon:9606"
// Aref="taxon:9606"
// Clone="InAMSE:2567826"
// Lab host="InAMSE:2567826"
// Lab host="InAMSE:2567826"
// Lab host="Organ: pooled; Vector: pT7T3D-pac (Pharmacia) with note="Organ: pooled; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDHL19W, testis NHT, and B-cell NCT_CGAP GCB1) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.B. Clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAG-TGTGTATGTAAAAGAACCTG 1051
                                                                                           1548 ATATICITICIGCATICATITITATAGCAACAACAATIGGTAAAACICACTGTGATCAAT 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 20-OCT-2000
   234 TGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAAGAC 175
                                                                                                                                                                                                                                                            114 ATATTGTTTCTGCATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAAT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2601 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 457.
                                                                                                                                  174 CAAGATITITCCTCTTGTGATTTCTTTAAAAGAATGACTATATAATTATTATTTCCACTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 AAAAGAATAGACAGAAACTCCATGCCAGTCGGTCGGT-AAAACAAACTCTTCCCAGGCCAA
                                                                                                                                                                                                                                                                                                                         ATTTTTATATCATGCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAA 1661
                                                                                                                                                                                                                                                                                                                                                        ATTTTTATATCATGCAAAATATGTTTAAAATAAATGAAAATTTTATTAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW070215
728 bp mRNA linear EST 20
xa09010.1. Soares NFL TGBC_S1 Homo saplens cDNA clone
IMAGE:256782 3' similar to SW:VBGC HUMAN P49767 VASCULAR
ENDOTHELIAL GROWTH FACTOR C PRECURSOR ;, mRNA sequence.
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Pred. No. 1.9e-99;
0; Mismatches 14;
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AW070215.1 GI:6025213
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larity 97.7%;
Conservative (
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Best Local Simi
Matches 708;
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AW070215/c
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TITLE
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                                                                                                                               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (infodimage.llnl.gov) for further information.
Insert Length: 785 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 476.
Seq primer: -40m12 fwd. ET from Amersham
High quality sequence stop: 476.

Incation/Qualifiers

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Contaction/Qualifiers
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Contac
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                         REFERENCE
AUTHORS
TITLE
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/MD xref="Lexxon:9606"
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/tissue_type="chandrosarcoma"
/tissue_type="chandrosarcoma"
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/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: Site_1: Ecor I;
Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
/note Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor; digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT) la tail. The sequence tag for this
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sequence: 1-53, >AT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
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99.5%; Pred. No. 1.2e-97;
M'amatches 3; Indels
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TAG_LIB=UI-H-EDO
TAG_SEQ=CGTCAAGGCT"
                                                                                                                                         /organism="Homo sapiens'
/mol_type="mRNA"
                                                                                      Location/Qualifiers
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Best Local S:
Matches 658
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UI-H-ED0-ayr-n-11-0-UI.S1 NCI_CGAP_ED0 Homo sapiens cDNA clone
IMAGE:5842762 3', mRNA sequence.
                                                                                                                                                                  GAAATGCTTGTTAAAAGGAAAGATCCTCCACCACCAAACATGCAGCTGTTACAGACGGCC 1171
                                                                                                                                                                                                                                                                    ATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTCG 1231
                                                                                                                                                                                                                                                                                                                                                                               TIGEGICCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCAGTT 1291
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Email: cgapbs-r@mail.nih.gov

Itsue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov

The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 370
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     GGTGGGGCAACCCGAGATTTGNATGAAAACACATGCCAGNTGTGTATGTAAAAGAACCTG 610
                                                                                                                                                                                                                                                                                                                            430
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                                                                                         CCCCAGARATCCACCCCTARARTCTGCCTGTARATGTGCCTGTGARATGTACCAGARAAGTCCCACA
                                                                                                                                                                                                 GAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACGGCC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-48, AT_rich#Low_complexity (matched compliment)
POLYA=Yes.
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                                                                          122 TITICIGCATICATITITATAGCAACAACAATIGGTAAAACTCACTGIGATCAATATITIT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 657) NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Length 657;

DB 13;

38.8%; Score 649;

Query Match

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Tissue Procurement: Christopher Moskaluk, M.D., Ph.
Emmert-Buck, M.D., Ph.D.
                                    Indels
ed. No. 1.8e-96;
Mismatches 5;
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Contact: Robert Strausberg, Ph.D.
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/mol_type="mRNN"
/db_xref="dataxon:9606"
/db_xref="dataxon:9606"
/tlssue type="carcinoid"
/tlssue type="carcinoid"
/lab_host="DA108"
/clone_lib="NCI_CGAP_Lu24"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 14,1791 and 15,20904-1522439). Subtraction by Bento Soares and M. Patima Bonaldo.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 TTGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGAC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 CAAATGAGCTAAGATTGTACTGTTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTG 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1020 AACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 AACACATGCCAGTGTGTATGT-AAAGAACCTGCCCAGGAAATCACCCCCTAAATCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080 AAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578 AAATGTGCTTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1320 TTGCCACAGTAGAACTGTCTGTGAACAGAGACCCCTTGTGGGTCCATGCTAACAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 AAAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1380 AAAAGICTGICTITCCTGAACCAIGTGGATAACTTTACAGAAATGGACTGGAGCTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1440 GCAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 cricicarricriraaagaargacrararaarrirarriccacraaaaararrcrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 GCAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%; Score 616; DB 10; Length 637; llarity 99.1%; Pred. No. 4.7e-91; Conservative 0; Mismatches 5; Indels
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Matches 630;
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/tissue_type="Lung"
//dev_etage="Adult and Fetal"
/lab_host="PulloB (Life Technologies) (TI phage resistant)"
/lab_host="PulloB (Life Technologies) (TI phage resistant)"
/lab_host="PulloB (Life Technologies) (TI phage resistant)"
/clome_lib="UI-CF-EGI"
/note="Organ: Lung, Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site]: ECOR is Site 2: Not I;
UI-CF-EGI is a normalized CDNA library contraining the following Issue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Scares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the editor.
CB854820 622 bp mRNA linear EST 22-APR-2003 UI-CF-EC1-ack-o-03-0-UI.S1 UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-ack-o-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1054 CCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCACAGA 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CNe Distribution: Researchers may obtain clones from Research
Generics (www.resgen.com).
The following repetitive elements were found in this CDNA
Seq prime: N. SAT rich#Low_complexity (matched compliment)
POLYA-Yes.
                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 622)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
721: 319 366 171
Fax: 319 356 7171
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/mol type="mENA"

/mol type="mENA"

/db xref="taxon:9606"

/clone="UI-CF-EC1 ack-o-03-0-UI"
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Pred. No. 7.9e-91;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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IAG_SEQ=None found"
                                                                                                                                                   CB854820.1 GI:30045199
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al Similarity 99.4%;
617; Conservative
                                                                                                                                                                                                                          Homo sapiens (human)
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829 ACTCATGCAGGGTGGCCTGTAAAA
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Local Similarity 84.5%;
les 731; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 916)
NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
High quality sequence stop: 620.
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                                                                                                        GTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCAGTTCA 1293
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AATGCTTGTTAAAAGGAAAGAGTTCCACCACCAAACATGCAGCTGTTACAGACGGCCAT 1173
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                                                                            GTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTGTCGTT
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                    562 AATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAACAACATGCAGCTGTTACAGACGGCCAT
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                                                    GTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTCGTT
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/mol_type="mRNA"
/db_xref="taxon:10090"
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BU510633,1 GI:22816866
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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/clone="IMAGE:6505339"
/tissue_type="undifferentiated limb"
/lab_hogt="DHIOB (phage-resistant)"
/clone_lib="NHI MGC 134"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site_2: NotI; Cloned undirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NHH_MGC Library."
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Pred. No. 5.7e-89;
0; Mismatches 115;
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/close libe.Melton Normalized Human Islet 4 N4-HIS 1."
/close libe.Melton Normalized Human Islet 4 N4-HIS 1."
/note="Organ: Pancreas; Vector: pSPORTI; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size selected by column
fractionation, average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
library. "Approxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

I (bases I to S84)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wile, R., Marten, J., Blistain, A.,
Schmitt, A., Theising, B., Kitter, E., Ronko, I., Bennett, J.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTS: 1e95f08.yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                  BM127186

BM127186

BM25184 bp mRNA linear BST 12-MAR-2002 15-95F08.xx Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5674886 3' similar to SW:VBGC HUMAN P49767

VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-857
Email: dmeltonobioth, harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Juliana Brown
(brown@fass.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
eng primer: -400P from Gibco.
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/dev_stage="Adult"
/lab_host="DH10B"
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/organism="Homo sapiens"
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High quality sequence stop: 448.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5674886"
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BM127186.1 GI:17121738
                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
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                                                                  LOCUS
DEFINITION
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VERSION
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584 TGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCAC 525
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                                                                   524 CACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGGCCA
                                                                                                                              1203 GGATTTTCATATAGTGAAGAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCACAA
                                                                                                                                                          464 GGATTTTCATATAGTGAAGAAGTGTGTTCGTTGTCCCTTCATATTGGAAAAGACCACAA
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                                                                                                                                                                                                                                                            404 ATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATTGAAAAACTGTGTTG
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                                          1143 CACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGCCA
                                                                                                                                                                                                                                                                                                        CCACAGTAGAACTGTCTGTGAACAGAGACCCTTGTGGGGTCCATGCTAACAAAGACAAA
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Search completed: February 25, 2004, 22:04:40 Job time : 4002 secs

Query Match 34.4%; Score 576; DB 12; Length 584; Best Local Similarity 99.1%; Pred. No. 1.7e-84; Matches 579; Conservative 0; Mismatches 5; Indels (

NIBING

1083

TGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCAC 1142

Gaps

. 0